

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:16:56 ; Search time 40 Seconds
(without alignments)
534.003 Million cell updates/sec

Title: US-09-867-159A-2
Perfect score: 1206
Sequence: 1 TNACSSINGNAPAEIDLQMR.....YFAANIDLMMEIBYPYVIL 222

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1144	94.9	245	2 JQ0337	allergen Der p 1 -
2	997.5	82.7	319	2 A61500	allergen Der f i p
3	982.5	81.5	211	2 S21864	probable cysteine
4	389.5	32.3	94	2 S03380	major fecal allerg
5	333.5	27.7	358	2 JC7787	carrot seed cystei
6	332	27.5	348	2 F84672	probable cysteine
7	327	27.1	367	2 JN0633	caricain (EC 3.4.2
8	327	27.1	367	2 JN0634	caricain (EC 3.4.2
9	326.5	27.1	326	2 T09259	cathepsin L-like p
10	323.5	26.8	329	2 JC2476	cathepsin K (EC 3.
11	322.5	26.7	374	2 T03941	cysteine proteinas
12	322	26.7	346	2 C96413	cysteine proteinas
13	322	26.7	362	1 S12581	cysteine proteinas
14	321	26.6	368	2 S47312	cysteine proteinas
15	321	26.6	465	2 T06416	cysteine proteinas
16	317.5	26.3	329	2 A49868	cathepsin K (EC 3.
17	315	26.1	215	2 A59428	ervatamin B (EC 3.
18	313	26.0	458	1 KHR20A	oryzain (EC 3.4.22
19	312.5	25.9	342	2 S71773	cysteine proteinas
20	311.5	25.8	312	2 A23705	cysteine proteinas
21	311.5	25.8	329	2 S74227	cathepsin K (EC 3.
22	311	25.8	221	2 A59041	cysteine proteinas
23	311	25.8	322	2 S19649	cysteine proteinas
24	310.5	25.7	380	1 TAGB	actinidain (EC 3.4
25	310	25.7	454	2 JC4848	cysteine proteinas
26	310.5	25.7	471	1 KHR20B	oryzain (EC 3.4.22
27	309.5	25.7	326	2 S43911	cathepsin L-like p
28	308.5	25.6	323	2 S19650	cysteine proteinas
29	308	25.5	365	2 T06206	probable cysteine

30	308	25.5	367	2 T12382	cysteine proteinas
31	307.5	25.5	345	2 T07839	anain (EC 3.4.22
32	307	25.5	352	2 T09760	chymopain (EC 3.
33	307	25.5	365	2 T06208	cysteine proteinas
34	307	25.5	367	2 T06529	cysteine proteinas
35	307	25.5	462	2 JN0719	drought-inducible
36	306	25.4	362	2 S22502	cysteine proteinas
37	305.5	25.3	356	2 T30426	cathpsin-like pro
38	304.5	25.2	302	2 S02728	actinidain (EC 3.4
39	304.5	25.2	325	2 S49451	cysteine proteinas
40	304.5	25.2	361	2 T06708	cysteine proteinas
41	304	25.2	313	2 S47433	cathepsin L (EC 3.
42	303.5	25.2	328	2 JQ1121	cysteine proteinas
43	303	25.1	348	2 T09798	glycyl endopeptida
44	303	25.1	349	2 T06207	cysteine proteinas
45	303	25.1	364	2 T46630	cysteine proteinas

ALIGNMENTS

RESULT 1
JQ0337
allergen Der p 1 - house-dust mite (Dermatophagoides pteronyssinus) (fragment)
C/Species: Dermatophagoides pteronyssinus
C/Date: 07-Sep-1990 #sequence,revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: JQ0337; A27582; A31657; C27634
R/Chua, K.Y.; Stewart, G.A.; Thomas, W.R.; Simpson, R.J.; Plozza, T.M.;
J. Exp. Med. 167, 175-182, 1988
A/Title: Sequence analysis of cDNA coding for a major house dust mite allergen, Der p 1:
A/Reference number: JQ0337; MUID:88089411; PMID:3335830
A/Accession: JQ0337
A/Molecule type: mRNA
A/Residues: 1-245 <CHU>
A/Cross-references: UNIPROT:P08176
R/Thomas, W.R.; Stewart, G.A.; Simpson, R.J.; Chua, K.Y.; Plozza, T.M.; Dilworth, R.J.;
Int. Arch. Allergy Appl. Immunol. 85, 127-129, 1988
A/Title: Cloning and expression of DNA coding for the major house dust mite allergen Der
A/Reference number: A27582; MUID:88114080; PMID:3276629
A/Accession: A27582
A/Molecule type: mRNA
A/Residues: 6-101 <THO>
A/Cross-references: GB:M24794; NID:G387591; PIDN:AAA28296.1; PID:G387592
R/Simpson, R.J.; Nice, E.C.; Moritz, R.L.; Stewart, G.A.
Protein Seq. Data Anal. 2, 17-21, 1989
A/Title: Structural studies on the allergen Der p1 from the house dust mite Dermatophago
A/Reference number: A31657; MUID:89098855; PMID:2911558
A/Accession: A31657
A/Status: preliminary
A/Molecule type: protein
A/Residues: 24-56,'XX',59-64;102-118;134-149;185-192,'X',194-200,'X',202 <SIM>
R/Lind, P.; Hansen, O.C.; Horn, N.
J. Immunol. 140, 4256-4262, 1988
A/Title: The binding of mouse hybridoma and human IgE antibodies to the major fecal alle
d by solid-phase inhibition assays with radiolabeled antigen.
A/Reference number: A92819; MUID:88229138; PMID:3372999
A/Accession: C27634
A/Molecule type: protein
A/Residues: 24-52 <LIN>
C/Superfamily: papain
C/Keywords: Glycoprotein
F;24-245/Product: allergen Der p 1 #status predicted <MAT>
F;75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.9% Score 1144; DB 2; Length 245;
Best Local Similarity 95.5% Pred. No. 1.5e-95;
Matches 212; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TNACSSINGNAPAEIDLQMRVTVPTRMQGGCGSCWAFSGVAATESAYLAHRNQLDLAEQ 60

Db 24 TNACSSINGNAPAEIDLQMRVTVPTRMQGGCGSCWAFSGVAATESAYLAHRNQLDLAEQ 83

Qy 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYTRYVAREQSCRPNQRRFGISNYCQIY 120

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Db      84  ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRVAREQSCRRPNAQRFGLSNYCQIY 143
      |||
Qy      121  PPVANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHNAVNIYGSNA 180
      |||
Db      144  PPVANKIREALAQPNQRYCHRYHTWIKDLDAFRHYDGRITIIQRDNGYQPNYHNAVNIYGSNA 203
      |||
Qy      181  QGVDDYWIVRNSWDTNWDGNGYGYFAANIDLMMIEEYPYVVIL 222
      |||
Db      204  QGVDDYWIVRNSWDTNWDGNGYGYFAANIDLMMIEEYPYVVIL 245
      |||

RESULT 2
A61500
allergen Der f I precursor - house-dust mite (Dermatophagoides farinae)
C:Species: Dermatophagoides farinae
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 26-Aug-1999
C:Accession: A61500
R:Dilworth, R.J.; Chua, K.Y.; Thomas, W.R.
C:Lin. Exp. Allergy 21, 25-32, 1991
A:Title: Sequence analysis of cDNA coding for a major house dust mite allergen, Der f I.
A:Reference number: A61500; MUID:91215493; PMID:2021874
A:Accession: A61500
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-319 <DIL>
A:Superfamily: papain

Query Match      82.7%; Score 997.5; DB 2; Length 319;
Best Local Similarity 81.2%; Pred. No. 3.2e-82;
Matches 181; Conservative 18; Mismatches 23; Indels 1; Gaps 1;

Qy      1  TNACSSING-NAPAEIDLQRMRTVTPIRMQGGCGSWAFSGVAATESAYLAHRNQSILDLAE 59
      |||
Db      97  TSACRINSVNVPSSELDLSRLTVPTRMQGGCGSWAFSGVAATESAYLAHRNQSILDLSE 156
      |||
Qy      60  QELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRVAREQSCRRPNAQRFGLSNYCQI 119
      |||
Db      157  QELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRVAREQSCRRPNSQHYGLSNYCQI 216
      |||
Qy      120  YPPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHNAVNIYGSN 179
      |||
Db      217  YPPDVQKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHNAVNIYGS 276
      |||
Qy      180  AQGVDDYWIVRNSWDTNWDGNGYGYFAANIDLMMIEEYPYVVIL 222
      |||
Db      277  TGGDDYWIVRNSWDTNWDGSGYGYFOAGNNLMMIEQYPYVWIM 319
      |||

RESULT 3
S21864
probable cysteine proteinase (EC 3.4.22.-) - Euroglyphus maynei
N:Alternate names: allergen Eur m I
C:Species: Euroglyphus maynei
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S21864
R:Kent, N.A.; Hill, M.; Keen, J.N.; Holland, P.W.H.; Hart, B.
submitted to the EMBL Data Library, June 1991
A:Reference number: S21864
A:Accession: S21864
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-211 <KEN>
A:Cross-references: UNIPROT:P25780; EMBL:X60073
C:Genetics:
A:Introns: 100/3; 155/2
C:Superfamily: papain
C:Keywords: cysteine proteinase; hydrolase

Query Match      81.5%; Score 982.5; DB 2; Length 211;
Best Local Similarity 83.9%; Pred. No. 4.3e-81;
Matches 177; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

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Qy      1  TNACSSING-NAPAEIDLQRMRTVTPIRMQGGCGSWAFSGVAATESAYLAHRNQSILDLAE 59
      |||
Db      1  TVACSSINSVLSSELDLSRLTVPTRMQGGCGSWAFSGVAATESAYLAHRNQSILDLAE 60
      |||
Qy      60  QELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRVAREQSCRRPNAQRFGLSNYCQI 119
      |||
Db      61  QELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRVAREQSCRRPNAQRYGLKNYCQI 120
      |||
Qy      120  YPPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHNAVNIYGSN 179
      |||
Db      121  SPDDSKIRQALQTHTAVAVIIGIKDLNAPFRHYDGRITIIQRDNGYQPNYHNAVNIYGSN 180
      |||
Qy      180  AQGVDDYWIVRNSWDTNWDGNGYGYFAANIDL 210
      |||
Db      181  TGGDDYWIVRNSWDTNWDGNGYGYFAANINL 211
      |||

RESULT 4
S03380
major fecal allergen Der p I - house-dust mite (Dermatophagoides pteronyssinus) (fragment)
N:Alternate names: allergen Der p1
C:Species: Dermatophagoides pteronyssinus
C>Date: 05-Mar-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S03380
R:Simpson, R.J.; Nice, E.C.; Moritz, R.L.; Stewart, G.A.
C:Protein Seq. Data Anal. 2, 17-21, 1989
A:Title: Structural studies on the allergen Der p1 from the house dust mite Dermatophagoides pteronyssinus
A:Reference number: A31657; MUID:89098855; PMID:2911558
A:Accession: S03380
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-28; 29-43; 44-60; 61-76; 77-94 <SIM>
A:Cross-references: UNIPROT:Q7M431
C:Superfamily: papain

Query Match      32.3%; Score 389.5; DB 2; Length 94;
Best Local Similarity 48.6%; Pred. No. 4.2e-28;
Matches 88; Conservative 0; Mismatches 4; Indels 89; Gaps 4;

Qy      1  TNACSSINGNAPAEIDLQRMRTVTPIR--MQGGCGSWAFSGVAATESAYLAHRNQSILDLA 58
      |||
Db      1  TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSXXAFSGVA----- 43
      |||
Qy      59  EQELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRVAREQSCRRPNAQRFGLSNYCQ 118
      |||
Db      44  -----GLEIYQHNGVQESY-----RFGISNYCQ 68
      |||
Qy      119  IYPPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHNAVNIYGS 178
      |||
Db      69  IYPPNANK-----DNGYQPNYXAVNIYGYX 93
      |||
Qy      179  N 179
      |||
Db      94  N 94
      |||

RESULT 5
JC7787
carrot seed cysteine proteinase (EC 3.4.-.-), CSCP - carrot
C:Species: Daucus carota (carrot)
C>Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004
C:Accession: JC7787
R:Sakuta, C.; Oda, A.; Konishi, M.; Yamakawa, S.; Kamada, H.; Satoh, S.
Biosci. Biotechnol. Biochem. 65, 2243-2248, 2001
A:Title: Cysteine proteinase gene expression in the endosperm of germinating carrot seeds
A:Reference number: JC7787
A:Contents: Seeds
A:Accession: JC7787
A:Molecule type: mRNA
A:Residues: 1-358 <SAK>
A:Cross-references: UNIPROT:Q948S1; DBJ:AB057371; DDBJ:AB057372
C:Comment: This protein is concerned with programmed cell death, and is endosperm-specific
C:Genetics:

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A;Gene: cscp
C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase
F;151,286,307/Active site: Cys, His, Asn #status predicted

Query Match 27.7%; Score 333.5; DB 2; Length 358;
Best Local Similarity 34.8%; Pred. No. 2.3e-22;
Matches 77; Conservative 87; Mismatches 21; Gaps 7;

QY 11 PABIDLRQMTVTPIRMQGGCGSWAFSGVAATESAYLAHRNOSLDLAEQELVDCASQ- 69
Db 128 PSSVDWEKKGAVPIKQKCGCGSWAFSAIVGVGKINKITNQLVLSLSEQLVDCESDNQ 187

QY 70 GCHGDTTPRGIEYIQHN-GVQSSYYRYVAREQSC--RRPNAQRFGISNVCQIYPPNANK 126
Db 188 GCNGGLMENALEFTKRSGGVTVTERVYPYRARDERCATKNAPVVKIDGHENVPENNEYA 247

QY 127 IREALAQTHSAIAVIGIKDLDAFRH--YDGRITIIQRDNGVQPNYHVNIVGV-SNAQGV 183
Db 248 LAQAVANQPVSVDAIDAGSDMQFYREGVYTGECGTELD-----HGVAVVGYGATNDGT 300

QY 184 DYWIVRNSWDTNMGDNGYGYFAANID-----LWMIIEYP 217
Db 301 KYWIVKNSWGTDMGRCYIEMVRDINAEGICGIAEASYP 341

RESULT 6
F84672
probable cysteine proteinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: F84672
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
eues, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84672
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <STO>
A;Cross-references: UNIPROT:Q9ZQH7; GB:AE002093; NID:94314384; PIDN:AAD15594.1; GSPDB:GN
C;Genetics:
A;Gene: At2g27420
A;Map position: 2
C;Superfamily: papain

Query Match 27.5%; Score 332; DB 2; Length 348;
Best Local Similarity 36.2%; Pred. No. 3e-22;
Matches 84; Conservative 32; Mismatches 86; Indels 30; Gaps 11;

QY 5 SINGNAPAEIDLROMRTVTPIRMQGGCGSWAFSGVAATESAYLAHRNOSLDLAEQELVD 64
Db 126 SDNGES---MDWRQEGAVTPVKYQCGCGSWAFSAVAAGITKTKGELVLSUSEQQLLD 182

QY 65 CASQH--GCHGDTTPRGIEY-IQHNQVQSSYYRYVAREQSCRRPNA-----QRFGISNY 116
Db 183 CDRDYNQCGRGKMSKAFVIKKNQGITTEDNPYQESQQTSSSTLSSFRATISGY 242

QY 117 CQIYPPNANKIREALAOQTHSAIAVIGIKDLDAFRHYDGRITIIQRDNGY--QPNYHVN 173
Db 243 -ETVPMNN---EEALLQAVSQPVSQVSGIEGTGAFRHYSQGVF-----NGBCGTDLHVAVT 294

QY 174 IVGYS-NAQGVVDYWIVRNSWDTNMGDNGYGYFAANID-----LWMIIEYP 217
Db 295 IVGYGMSSEGTGYWVVKNSWGTWNGYMRIRKRDVDAPQGMCGLATIATFP 346

RESULT 7
JN0633
caricain (EC 3.4.22.30) I precursor - papaya
N;Alternate names: papaya proteinase omega I; peptidase A; peptidase II; proteinase A; p

C;Species: Carica papaya (papaya)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JN0633; S01135; S11748; A43026; S35728
R;Revell, D.F.; Cummings, N.J.; Baker, K.C.; Collins, M.E.; Taylor, M.A.J.; Sumner, I.G.
Gene 127, 221-225, 1993
A;Title: Nucleotide sequence and expression in Escherichia coli of cDNAs encoding papaya
A;Reference number: JN0633; MUID:93273235; PMID:7684720
A;Accession: JN0633
A;Molecule type: mRNA
A;Residues: 1-348 <REV>
A;Cross-references: UNIPROT:P10056; EMBL:X66060; NID:g18097; PIDN:CAA46862.1; PID:g18098
A;Experimental source: fruit and leaf
R;Dubois, T.; Kleinschmidt, T.; Schneek, A.G.; Looze, Y.; Braunitzer, G.
Biol. Chem. Hoppe-Seyler 369, 741-754, 1988
A;Title: The thiol proteinases from the latex of Carica papaya L. II. The primary structure
A;Reference number: S01135; MUID:89105320; PMID:3063283
A;Accession: S01135
A;Molecule type: protein
A;Residues: 133-348 <DUB>
R;Collins, M.E.; Revell, D.F.; Sumner, I.G.; Pickersgill, R.W.; Goodenough, P.W.
submitted to the EMBL Data Library, February 1990
A;Reference number: S11748
A;Accession: S11748
A;Molecule type: mRNA
A;Residues: 237-348 <COL>
A;Cross-references: EMBL:X51899; NID:g18095; PIDN:CAA36180.1; PID:gl360713
C;Genetics:
A;Gene: Pp-omega
C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase
F;15-132/Domain: signal sequence #status predicted <SIG>
F;15-132/Domain: propeptide #status predicted <PRO>
F;133-348/Product: caricain #status experimental <MAT>
F;154-195,188-227,285-336/Disulfide bonds: #status predicted
F;157,291,311/Active site: Cys, His, Asn #status predicted

Query Match 27.1%; Score 327; DB 2; Length 348;
Best Local Similarity 37.2%; Pred. No. 8.4e-22;
Matches 74; Conservative 34; Mismatches 77; Indels 14; Gaps 7;

QY 9 NAPAETDLROMRTVTPIRMQGGCGSWAFSGVAATESAYLAHRNOSLDLAEQELVDCASQ 68
Db 132 NLPENVDWRKKGAVTPVRHQGCGCGSWAFSAVATVEGINKIRTKLVSEQLVDCERR 191

QY 69 -HCHGDTTPRGIEYIQHNQVQSSYYRYVAREQSCRRPNAQRFG-----ISNYCQIYPP 122
Db 192 SHGCKGKGYPPYALEYVAKNGIHLRSKYPYKAKQGTCK--AKQVGGPIVKTSGVGRVQPN 248

QY 123 NANKIREALAOQTHSAIAVIGIKDLDAFRHYDGRITIIQRDNGVQPNYHVNIVGYSNAQ 182
Db 249 NEGNLLNATAK--QPVSVVVESKG-RPFQLYKG-GIFEGPCGTKVD-HAVTAVGVGKSGG 303

QY 183 VDYWIVRNSWDTNMGDNGY 201
Db 304 KGVILKNSWGTANGKGY 322

RESULT 8
JN0634
caricain (EC 3.4.22.30) II precursor - papaya
N;Alternate names: papaya proteinase omega II
C;Species: Carica papaya (papaya)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JN0634; A43027; S31823
R;Revell, D.F.; Cummings, N.J.; Baker, K.C.; Collins, M.E.; Taylor, M.A.J.; Sumner, I.G.
Gene 127, 221-225, 1993
A;Title: Nucleotide sequence and expression in Escherichia coli of cDNAs encoding papaya
A;Reference number: JN0633; MUID:93273235; PMID:7684720
A;Accession: JN0634
A;Molecule type: mRNA
A;Residues: 1-367 <REV>
A;Cross-references: UNIPROT:Q42673; EMBL:X69877; NID:922660; PIDN:CAA49504.1; PID:g22661
A;Experimental source: fruit and leaf

C:Genetics:
A:Gene: Pp-omega
C:Superfamily: papain
C:Keywords: cysteine proteinase; hydrolase
F:1-11/Domain: signal sequence #status predicted <SIG>
F:12-132/Domain: propeptide #status predicted <PRO>
F:133-367/Product: carlacin II #status predicted <MAT>
F:154-195,188-227,285-336/Diulfide bonds: #status predicted
F:157,291,311/Active site: Cys, His, Asn #status predicted

Query Match 27.1%; Score 327; DB 2; Length 367;
Best Local Similarity 37.2%; Pred. No. 9e-22;
Matches 74; Conservative 34; Mismatches 77; Indels 14; Gaps 7;

QY 9 NAPAELDLQMTVTPIRMQGGSCWAFSGVAATESAYLAHRNQSLLDLAEQLVDCASQ 68
DB 132 NLPENVDWRKGAVTPIRQGGSCWAFSAVATVEGINKIRTKGLVELSEQLVDCERR 191
QY 69 -HGCHGDTIPRGIEYIOHNGVQESYRYVAREQSCRRPNAQRFQ-----ISNYCQIYPP 122
DB 192 SHGCKGGYPYALEYVAKNGIHLRSKYPYKAKQGTCTCR---AKQVGGPIVKTSGVGRVQPN 248
QY 123 NANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTHIQRDNGYQPNYHVNIVGYSNAQG 182
DB 249 NEGNLLNATAK--QPVSVVVESKG-RPFQLYKG-GIFEGPCGTQVD-HAVTAVGYKSGG 303
QY 183 VDIWIVRNSWDTNWGDNGY 201
DB 304 KGYILKNSWGTAWGEGY 322

RESULT 9
T02959
cathepsin L-like proteinase (EC 3.4.22.-) - liver fluke
C:Species: Fasciola hepatica (liver fluke)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09259
R:Heussler, V. T.; Dobbelaere, D. A. E.
Mol. Biochem. Parasitol. 64, 11-23, 1994
A:Title: Cloning of a proteinase gene family of Fasciola hepatica by polymerase chain reaction
A:Reference number: T16631; MUID:94359526; PMID:8078514
A:Accession: T09259
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-326 <HEU>
A:Cross-references: UNIPROT:Q24944; EMBL:Z22765; NID:9452257; PID:9452258
C:Superfamily: papain
C:Keywords: cysteine proteinase; hydrolase
F:132,269,289/Active site: Cys, His, Asn #status predicted

Query Match 27.1%; Score 326.5; DB 2; Length 326;
Best Local Similarity 34.4%; Pred. No. 8.7e-22;
Matches 72; Conservative 31; Mismatches 83; Indels 23; Gaps 5;

QY 11 PAEIDLQMTVTPIRMQGGSCWAFSGVAATESAYLAHRNQSLLDLAEQLVDCASQ---S 67
DB 109 PESIDNRDYYTEVKDQKQGGSCWAFSTTGAVGQFRKNERASFSQQLVDCTRDFG 168
QY 68 QHCHGDTIPRGIEYIOHNGVQESYRYVAREQSCRRPNAQRFQ-ISNYCQIYPPNANK 126
DB 169 NYGCGGGYMEAYELKHNGLETESYYPYQAVEGPGQYDGLAYAKVTGYTYVHSGDEIE 228
QY 127 IREALAQTHSAIAVIIGIKDLDAFR-HYDGRTHIQRDNGYQPN-----YHAVNIVGYS 178
DB 229 LKN-----LVGTEDLPAVALDADSDFMYSQGIYQSGTCLPDLRTHAVLAVGYG 277
QY 179 NAQGVDIWIVRNSWDTNWGDNGYGYFAAN 207
DB 278 SQDGTDIWIVKNSWGTWGEDGYIRFARN 306

RESULT 10
JC2476

cathepsin K (EC 3.4.22.-) precursor - human
N:Alternate names: cathepsin O2
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C:Accession: JC2476; S55763; S68459; I38752; S48830
R:Inaoka, T.; Bilbe, G.; Ishibaashi, O.; Tezuka, K.; Kumegawa, M.; Kokubo, T.
Biochem. Biophys. Res. Commun. 206, 89-96, 1995
A:Title: Molecular cloning of human cDNA for cathepsin K: Novel cysteine proteinase predicted
A:Reference number: JC2476; MUID:95118380; PMID:7818555
A:Accession: JC2476
A:Molecule type: mRNA
A:Residues: 1-329 <INA>
A:Cross-references: UNIPROT:P43235; EMBL:X82153; NID:9562756; PIDN:CAA57649.1; PID:9562756
R:Broemme, D.; Okamoto, K.
Biol. Chem. Hoppe-Seyler 376, 379-384, 1995
A:Title: Human cathepsin O2, a novel cysteine protease highly expressed in osteoclastoma
A:Reference number: S55763; MUID:96082523; PMID:7576232
A:Accession: S55763
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-329 <BRO>
A:Cross-references: GB:S79895; NID:9135555; PIDN:AAB35521.1; PID:91195556
R:Shi, G. P.; Chapman, H. A.; Bhairi, S. M.; Deleeuw, C.; Reddy, V. Y.; Weiss, S. J.
FEBS Lett. 357, 129-134, 1995
A:Title: Molecular cloning of human cathepsin O, a novel endoproteinase and homologue of
A:Reference number: I38752; MUID:95104457; PMID:7805878
A:Accession: S68459
A:Molecule type: mRNA
A:Residues: 1-329 <SHI>
A:Cross-references: EMBL:U13665; NID:9606922; PIDN:AAA65233.1; PID:9606923
A:Experimental source: tissue-type blood
C:Genetics:
A:Gene: GDB:CTSK; PYCD; CTSO1; CTSO2; PKND; CTSO
A:Cross-references: GDB:453910; OMIM:265800; OMIM:601105
A:Map position: 1q21-q21
C:Superfamily: papain
C:Keywords: cysteine proteinase; glycoprotein; hydrolase
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-114/Domain: propeptide #status predicted <PRO>
F:115-329/Product: cathepsin K #status predicted <MAT>
F:133,161,213/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:139,276,296/Active site: Cys, His, Asn #status predicted

Query Match 26.8%; Score 323.5; DB 2; Length 329;
Best Local Similarity 36.0%; Pred. No. 1.6e-21;
Matches 73; Conservative 30; Mismatches 95; Indels 5; Gaps 5;

QY 8 GNAPAEIDLQMTVTPIRMQGGSCWAFSGVAATESAYLAHRNQSLLDLAEQLVDCAS 67
DB 113 GRAPDSVDYRKGYVTPIRQGGSCWAFSGVAATESAYLAHRNQSLLDLAEQLVDCVS 172
QY 68 QH-GCHGDTIPRGIEYIOHNGVQESYRYVAREQSCRRPNAQRFQISNYCQIYPPNA 124
DB 173 ENDGCGGGYMTWAFQYVQKNRGIDSEDAIYYPYQVEESCMYNPPTGKAACRCGYREIPEGNE 232
QY 125 NKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTHIQRDNGYQPNYHVNIVGYSNAQGV 184
DB 233 KALKAVARV-GPVSVAID-ASLTGFQYKSGYGYDESCNLDNLNHLAVLAVGYGKGNK 290
QY 185 YWIVRNSWDTNWGDNGYGYFAAN 207
DB 291 HWIKNSWGNKNGYILMARN 313

RESULT 11
T03941
cysteine proteinase (EC 3.4.22.-) precursor - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T03941
R:Becker, C.; Muentz, K.
A:Description: cDNA cloning of a CPRI-homologous proteinase from germinating tobacco seed


```

QY    98 AREQSRRRPAQRFGISNYCQIYPNANKIRREALAQTHTSAIAVIGIKDLDA----FRHY 153
      :|||:::||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db   221 VKEGPCRSNARPAILLRGFENVPNNERALLAEAVSRQPVAVAL-----DASEAGFVHY 273
      :|||:::||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY    154 DGETIIQRONGQPNHNAHVNGV-SNAOGVDWIIVRNWDWTWGDNGY 201
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db   274 SGGVYNARNCGTSVN-HAVTLVGYGTSPEGMKYWLAKNSWGKTGNGSY 321
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:


RESULT 13
SI2581
cysteine proteinase (EC 3.4.22.-) precursor - black gram
N;Alternate names: cysteine endopeptidase; sulphydryl endopeptidase
C;Species: Vigna mungo (black gram)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: SI2581; S05497; S20213; S48684
R;Akasofu, H.; Yamauchi, D.; Minamikawa, T.
Nucleic Acids Res. 18, 1892, 1990
A;Title: Nucleotide sequence of the gene for the Vigna mungo sulphydryl-endopeptidase (S)
A;Reference number: SI2581; MUID:90245586; PMID:2336365
A;Accession: SI2581
A;Molecule type: DNA
A;Residues: 1-362 <AA>
A;Cross-references: UNIPROT:P12412; EMBL:X51900; NID:g22065; PIDN:CAA36181.1; PID:g22066
R;Akasofu, H.; Yamauchi, D.; Mituhashi, W.; Minamikawa, T.
Nucleic Acids Res. 17, 6733, 1989
A;Title: Nucleotide sequence of cDNA for sulphydryl-endopeptidase (SH-Ep) from cotyledon
A;Reference number: S05497; MUID:89386007; PMID:2780300
A;Accession: S05497
A;Molecule type: mRNA
A;Residues: 1-362 <AA>
A;Cross-references: EMBL:X15732; NID:g22061; PIDN:CAA33753.1; PID:g22062
A;Accession: S20213
A;Molecule type: protein
A;Residues: 132-140 <AA>
R;Okamoto, T.; Nakayama, H.; Seto, K.; Isobe, T.; Minamikawa, T.
FEBS Lett. 351, 31-34, 1994
A;Title: Posttranslational processing of a carboxy-terminal propeptide containing a KDE
A;Reference number: S48684; MUID:94357273; PMID:8076688
A;Accession: S48684
A;Molecule type: protein
A;Residues: 127-140/197-216/324-333/339-352 <OK>
C;Genetics:
A;Introns: 150/1; 228/3; 275/3
C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase
F;1-20/Domains: signal sequence #status predicted <SIG>
F;21-362/Product: cysteine proteinase #status predicted <MAT>
F;152,288,309/Active site: Cys, His, Asn #status predicted

Query Match          26.7%; Score 322; DB 1; Length 362;
Best Local Similarity 35.0%; Pred.No. 2.5e-21;
Matches       78; Conservative 33; Mismatches 94; Indels 18; Gaps 8;

QY    8 GNAPABIDLQRMRTVTPIRMQGCGSCWAFFSGVAATESAYLAHRNQSLDLAQELVDCAS 67
Db   126 GSVPASVDWRKKGAFTDVKDGQCSCWAFFSTIVAVEGINQTKNLVLSIQEVLVCDCK 185

QY    68 Q--HGCHGTDPGRIBVI-QHNQGVQESYYRVAREQSC--RRPNAQRFGISNYCQIYPP 122
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db   186 EENQCNCGGLMESAFEFIKQGGITTTESNPYPTAOBCTDESKVNDLAVSIDGHENPVVN 245

QY    123 NANKIREALQAOTHSATAVIIIGIKDLDAFRHYDRTIIQRDNQGPQNHYNAVTVGY-SNAQ 181
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db   246 DENALKLVANQPSVAIDDGSD---FOFY-SEGVTGDCNTDLM-HGVAIVGYGTTVD 300

QY    182 GDVDYTIVRNSWDTNWGDNGYGFYAANID-----LMMTIEEP 217
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db   301 GTINYIIVNRNSWGPENGQEQQGIYRMQRNISKEGCLGITAMMASYP 343

RESULT 14
```

S47312
cysteine proteinase (EC 3.4.22.-) precursor - spring vetch
C:Species: Vicia sativa (spring vetch, tare)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S51817; S47312
R/Becker, C.; Fischer, J.; Nong, V.H.; Muenitz, K.
Plant Mol. Biol. 26, 1207-1212, 1994
A>Title: PCR cloning and expression analysis of cDNAs encoding cysteine proteinases from
A/Reference number: S51817; MUID:95111103; PMID:7811978
A/Accession: S51817
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-368 <BE2>
A/Cross-references: UNIPROT:O41696; EMBL:X75749; NID:G535472; PIDN:CAA53377.1; PID:G5354
A/Note: the authors translated the codon GAT for residue 241 as Glu
C/Superfamily: papain
C/Keywords: cysteine proteinase; hydrolase
F:152,288,308/Active site: Cys, His, Asn #status predicted

Query Match 26.6%; Score 321; DB 2; Length 368;
Best Local Similarity 35.1%; Pred. No. 3.1e-21;
Matches 72; Conservative 34; Mismatches 85; Indels 14; Gaps 5;

QY 11 PAEIDLQRMRTVPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQELVDC--ASQ 68
DB 129 PVHVDWRLKGAITHIKDQSGCGSCWAFSTIATVEAINKIWTGKLVSLSEQLVDCDRAFN 188
QY 69 HGCHGDTIPRGIEYIOHNGVQ-ESYRYVAREQSC--RRPNAQRFGISNYCOIYPPNAN 125
DB 189 EGCNGGLMDYAFEFIINGGGIDTDQHPYKGFEGRCDDPTKKAKIVSIDGYEDVPSNNEN 248
QY 126 KIREALAQTHSAIAVIIGIKDIDAFRH--YDGRITIQRDNGYQPNYHAVNIVGYSNAQGV 183
DB 249 ALKKAHAHQVPSVAIEASGALQLYSGVFTGKCTSLD-----HAVVIVGYGSEGL 301
QY 184 DYWIVRNSWDTNMGDNGYGYFAANI 208
DB 302 DYWLVRNSWGTNMGEDGYFKMERNV 326

RESULT 15
T06416
cysteine proteinase (EC 3.4.22.-) precursor - tomato
C:Species: Lycopersicon esculentum (tomato)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T06416
R/Lers, A.
submitted to the EMBL Data Library, December 1997
A/Reference number: Z15662
A/Accession: T06416
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-466 <LER>
A/Cross-references: UNIPROT:O49877; EMBL:AJ003137; PIDN:CAA05894.1
A/Experimental source: cultivar Cherry
C/Genetics:
A/Gene: C14
C/Superfamily: papain
C/Keywords: cysteine proteinase; hydrolase
F:162,298,318/Active site: Cys, His, Asn #status predicted

Query Match 26.6%; Score 321; DB 2; Length 466;
Best Local Similarity 36.9%; Pred. No. 4.1e-21;
Matches 76; Conservative 28; Mismatches 82; Indels 20; Gaps 6;

QY 6 INGNPAEIDLQRMRTVPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQELVDC 65
DB 134 VGDSPESIDWREKGLVGVKDGQSGCGSCWAFSAVAAMESINAIVTGNLISLSEQLVDC 193
QY 66 --ASQHGCHGDTIPRGIEY-IQHNQVVQESYRYVAREQSC--RRPNAQRFGISNYCOIY 120
DB 194 DRSYNEGCGGLMDYAFEFVIRKNIGGIDTDEDPYKERNVCDQYRKNKAVKVIDSYEDVP 253

QY 121 PPNANKIREALAQTHSAIAVIIGIKDIDAFRH-----DGRITIQRDNGYQPNYHAVNIV 175
DB 254 VVNEKALQKAVAHQVPSIALEAGRD---FQHYKSGIFTGKCGTAYD-----HGVVIA 303
QY 176 GYSNAQGVVDYWIIVRNSWDTNMGDNGY 201
DB 304 GYGTENGMDYWIIVRNSWGANWGENGY 329

Search completed: May 19, 2005, 17:23:28
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:13:36 ; Search time 60 Seconds
(without alignments)
1894.693 Million cell updates/sec

Title: US-09-867-159a-2

Perfect score: 1206

Sequence: 1 TNACSGNGAPAEIDLQMR.....YFAANIDLMIEBPYVIL 222

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1196	99.2	320	1	MMAL_DERPT	P08176 dermatophag
2	1037.5	86.0	321	1	RUMI_EURMA	P25780 euroglyphus
3	997.5	82.7	321	1	MMAL_DERFA	P16311 dermatophag
4	944.5	78.3	210	2	O9GY70	O9GY70 dermatophag
5	607	50.3	146	2	O95X05	O95X05 dermatophag
6	591.5	49.0	263	2	O8I9P1	O8I9P1 psoroptes o
7	469	38.9	107	2	O95X04	O95X04 dermatophag
8	437	36.2	133	2	O968Y3	O968Y3 dermatophag
9	389.5	32.3	94	2	O7M431	O7M431 dermatophag
10	382	31.7	221	2	O95P04	O95P04 blomia trop
11	341.5	28.3	333	2	O7SX07	O7SX07 petromyzon
12	332.5	27.6	366	2	O6ZHP9	O6ZHP9 oryza sativ
13	332	27.5	348	2	O9ZQH7	O9ZQH7 arabidopsis
14	331	27.4	326	2	O7I7S6	O7I7S6 callosobruc
15	330.5	27.4	393	2	O6E7B4	O6E7B4 brugia mala
16	328.5	27.2	326	2	O6T857	O6T857 fasciola gi
17	328.5	27.2	460	2	O7XXU7	O7XXU7 anthurium a
18	328	27.2	362	2	O7X7A6	O7X7A6 glycine max
19	327.5	27.2	395	1	CATL_BRUPA	O17473 brugia paha
20	327	27.1	348	1	PAP3_CARPA	P10056 carica papa
21	327	27.1	367	2	O42673	O42673 carica papa
22	326.5	27.1	326	2	O24944	O24944 fasciola he
23	326.5	27.1	327	2	O6QXF0	O6QXF0 agrotis seg
24	326	27.0	326	2	O7I7S5	O7I7S5 callosobruc
25	325	26.9	326	2	O7I7S9	O7I7S9 callosobruc
26	324.5	26.9	326	2	O7JN08	O7JN08 fasciola he
27	324	26.9	326	2	O7I7T0	O7I7T0 callosobruc
28	324	26.9	370	2	O9XF79	O9XF79 sandersonia
29	323.5	26.8	329	1	CATK_HUMAN	P43235 homo sapien
30	323.5	26.8	329	1	CATK_MACFA	P61276 macaca fasc
31	323.5	26.8	329	1	CATK_MACMU	P61277 macaca mula

32 323.5 26.8 329 2 Q6FHN2 Q6fhn2 homo sapien
33 323 26.8 323 2 Q86GF7 Q86gf7 pandalus bo
34 323 26.8 326 2 Q717S1 Q717s1 callosobruc
35 323 26.8 462 2 Q93XQ9 Q93xq9 ipomoea bat
36 322.5 26.7 326 2 Q717S4 Q717s4 callosobruc
37 322.5 26.7 326 2 Q9NGW2 Q9ngw2 fasciola gi
38 322.5 26.7 374 2 Q24137 Q24137 nicotiana t
39 322 26.7 337 2 Q7YXL3 Q7yxl3 tenebrio m
40 322 26.7 346 2 O9LFP9 O9lfp9 arabidopsis
41 322 26.7 362 1 CYSP VIGMU P12412 vigna mungo
42 321.5 26.7 445 2 O8W182 O8w182 brassica ol
43 321 26.6 368 2 O41696 O41696 vicia sativ
44 321 26.6 400 2 Q9BJM2 Q9bjm2 litomosoid
45 321 26.6 466 2 O49877 O49877 lycopersico

ALIGNMENTS

RESULT 1
MMAL_DERPT ID_MMAL_DERPT STANDARD; PRT; 320 AA.
AC P08176; Q24616;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Major mite fecal allergen Der p 1 precursor (EC 3.4.22.-) (Der p 1).
GN Name=DERP1;
OS Dermatophagoides pteronyssinus (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
OC Pyroglyphidae; Dermatophagoides.
OX NCBI_TaxID=6956;
RN [1]
RP SEQUENCE FROM N.A., AND POLYMORPHISM.
RX MEDLINE=93357682; PubMed=8353459;
RA Chua K.Y., Kehal P.K., Thomas W.R.;
RT "Sequence polymorphisms of cDNA clones encoding the mite allergen Der p 1.";
RL Int. Arch. Allergy Immunol. 101:364-368(1993).
RN [2]
RP SEQUENCE OF 76-320 FROM N.A.
RX MEDLINE=88089411; PubMed=3335830;
RA Chua K.Y., Stewart G.A., Thomas W.R., Simpson R.J., Dilworth R.J., Plozza T.M., Turner K.J.;
RT "Sequence analysis of cDNA coding for a major house dust mite allergen, Der p 1. Homology with cysteine proteases.";
RL J. Exp. Med. 167:175-182(1988).
RN [3]
RP SEQUENCE OF 81-176 FROM N.A.
RX MEDLINE=88114080; PubMed=3276629;
RA Thomas W.R., Stewart G.A., Simpson R.J., Chua K.Y., Plozza T.M., Dilworth R.J., Nisbet A., Turner K.J.;
RT "Cloning and expression of DNA coding for the major house dust mite allergen Der p 1 in Escherichia coli.";
RL Int. Arch. Allergy Appl. Immunol. 85:127-129(1988).
RN [4]
RP REVISIONS TO 232-241.
RX MEDLINE=91215493; PubMed=2021874;
RA Dilworth R.J., Chua K.Y., Thomas W.R.;
RT "Sequence analysis of cDNA coding for a major house dust mite allergen, Der p 1.";
RL Clin. Exp. Allergy 21:25-32(1991).
RN [5]
RP SEQUENCE OF 99-308 FROM N.A.
RX MEDLINE=93130112; PubMed=1483062;
RA Kent N.A., Hill M.R., Keen J.N., Holland P.W., Hart B.J.;
RT "Molecular characterization of group I allergen Eur m 1 from house dust mite Euroglyphus maynei.";
RL Int. Arch. Allergy Immunol. 99:150-152(1992).
RN [6]
RP SEQUENCE OF 99-127.
RX MEDLINE=88229138; PubMed=3372999;

```

RA Lind P., Hansen O.C., Horn N.;
RT "The binding of mouse hybridoma and human IgE antibodies to the major
RT fecal allergen. Der p 1, of Dermatophagoides pteronyssinus. Relative
RT binding site location and species specificity studied by solid-phase
RT inhibition assays with radiolabeled antigen."
RL J. Immunol. 140:4256-4262(1988).
RN [7]
RP SEQUENCE OF 99-139; 177-192; 208-224 AND 260-277, AND VARIANT ALA-222.
RX PubMed=2911558;
RA Simpson R.J., Nice E.C., Moritz R.L., Stewart G.A.;
RT "Structural studies on the allergen Der p1 from the house dust mite
RT Dermatophagoides pteronyssinus: similarity with cysteine
RT proteinases."
RN Protein Seq. Data Anal. 2:17-21(1989).
RP [8]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=95062135; PubMed=7971950;
RA Topham C.M., Srinivasan N., Thorpe C.J., Overington J.P.,
RA Kalsheker N.A.;
RT "Comparative modelling of major house dust mite allergen Der p 1:
RT structure validation using an extended environmental amino acid
RT propensity table."
RL Protein Eng. 7:869-894(1994).
CC -1- FUNCTION: Thiol protease that hydrolyzes proteins, with a
CC preference for Phe or basic residues.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALLERGEN: Causes an allergic reaction in human. Common symptoms of
CC mite allergy are bronchial asthma, allergic rhinitis and
CC conjunctivitis. Reacts with IgE in 80% of patients with house dust
CC allergy.
CC -1- SIMILARITY: Belongs to the peptidase C1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U11695; AAB60215.1; -.
DR EMBL; M24794; AAA28296.1; ALT_INIT.
DR EMBL; X65197; CAA46317.1; -.
DR PIR; JQ0337; JQ0337.
DR HSSP; P53634; IK3B.
DR MEROPS; C01.073; -.
DR InterPro; IPR000169; Pept_cys_actsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00845; Pept_C1; 1.
DR PROSITE; PS00640; THIOL_PROTEASE ASN; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
DR Allergen; Direct protein sequencing; Glycoprotein; Hydrolase;
KW Polymorphism; Signal; Thiol protease; Zymogen.
FT SIGNAL 1 18 Potential.
FT PROPEP 19 98 Activation peptide.
FT CHAIN 99 320 Major mite fecal allergen Der p 1.
FT CARBOHYD 150 150 N-linked (GlcNAc...) (Potential).
FT ACT_SITE 132 132 By similarity.
FT ACT_SITE 268 268 By similarity.
FT ACT_SITE 288 288 By similarity.
FT DISULFID 102 215 By similarity.
FT DISULFID 129 169 By similarity.
FT DISULFID 163 201 By similarity.
FT VARIANT 148 148 Y -> H.
FT VARIANT 179 179 E -> K.
FT VARIANT 222 222 V -> A.
FT VARIANT 234 234 S -> T.
FT VARIANT 313 313 E -> Q.
SQ SEQUENCE 320 AA; 36104 MW; A0B1P4DD09791DFE CRC64;

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Query Match 99.2%; Score 1196; DB 1; Length 320;
Best Local Similarity 99.1%; Pred.No. 4.9e-99;
Matches 220; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TNACSGINGNAPAEIDLRQMTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
DB 99 TNACSGINGNAPAEIDLRQMTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLLAEQ 158
QY 61 ELVDCASQHCCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRRQAORFGISNYCQIY 120
DB 159 ELVDCASQHCCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRRQAORFGISNYCQIY 218
QY 121 PNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITTIQRDNGYQPNYHVNIVGYSNA 180
DB 219 PNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITTIQRDNGYQPNYHVNIVGYSNA 278
QY 181 QGVYDWIVRNSWDTNNGDNGYGYFAANIDLMIMEEYPYVVIL 222
DB 279 QGVYDWIVRNSWDTNNGDNGYGYFAANIDLMIMEEYPYVVIL 320

RESULT 2
EUN1_EURMA STANDARD; PRT; 321 AA.
ID EUN1_EURMA STANDARD; PRT; 321 AA.
AC P25780; Q9TZ23; Q9T224; Q9UBA0;
DT 01-MAY-1992 (Rel. 22, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Mite group 1 allergen Eur m 1 precursor (EC 3.4.22.-) (Eur m I).
GN Name=EURM1;
OS Eurygllyphus maynei (Wayne's house dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcotiformes; Astigmata; Psoroptidia; Analgoidea;
OC Pyroglyphidae; Eurygllyphus.
OX NCBI_TaxID=6958;
RN [1]
RP SEQUENCE FROM N.A. (EUR M 1.0101 AND EUR M 1.0102).
RX MEDLINE=99126275; PubMed=9925958; DOI=10.1159/000024026;
RA Smith W., Mills K., Hazell L., Hart B.J., Thomas W.;
RT "Molecular analysis of the group 1 and 2 allergens from the house dust
RT mite, Eurygllyphus maynei."
RL Int. Arch. Allergy Immunol. 118:15-22(1999).
RN [2]
RP SEQUENCE OF 99-309 FROM N.A.
RX MEDLINE=93130112; PubMed=1483062;
RA Kent N.A., Hill M.R., Keen J.N., Holland P.W., Hart B.J.;
RT "Molecular characterisation of group 1 allergen Eur m 1 from house
RT dust mite Eurygllyphus maynei."
RL Int. Arch. Allergy Immunol. 99:150-152(1992).
CC -1- FUNCTION: Probable thiol protease.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALLERGEN: Causes an allergic reaction in human. Common symptoms of
CC mite allergy are bronchial asthma, allergic rhinitis and
CC conjunctivitis.
CC -1- SIMILARITY: Belongs to the peptidase C1 family.
CC -----
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CC -----
DR EMBL; AF047610; AAC82351.1; -.
DR EMBL; AF047611; AAC82352.1; ALT_INIT.
DR EMBL; AF047612; AAC82353.1; -.
DR EMBL; X60073; CAA42677.1; -.
DR PIR; S21864; S21864.
DR HSSP; P53634; IK3B.
DR MEROPS; C01.073; -.
DR InterPro; IPR000169; Pept_cys_actsite.

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DR InterPro; IPR000668; Peptidase C1.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPA1N.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept C1; 1.
DR PROSITE; PS00640; THIOI_PROTEASE ASN; 1.
DR PROSITE; PS00139; THIOI_PROTEASE CYS; 1.
DR PROSITE; PS00639; THIOI_PROTEASE HIS; 1.
KW Allergen; Glycoprotein; Hydrolase; Signal; Thiol protease; Zymogen.
FT SIGNAL 1 18 Potential.
FT PROPEP 19 98 Mite group 1 allergen Eur m 1.
FT CHAIN 99 321 By similarity.
FT ACT_SITE 133 133 By similarity.
FT ACT_SITE 269 269 By similarity.
FT ACT_SITE 289 289 By similarity.
FT DISULFID 130 170 By similarity.
FT CARBOHYD 34 34 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).
FT VARIANT 36 36 T -> S (in Eur m 1.0102).
FT VARIANT 126 126 M -> N (in Eur m 1.0102).
FT VARIANT 320 320 M -> I (in Eur m 1.0102).
SQ SEQUENCE 321 AA; 36290 MW; 6CFD44FEC725999E CRC64;

Query Match 86.0%; Score 1037.5; DB 1; Length 321;
Best Local Similarity 85.9%; Pred. No. 8.4e-85;
Matches 181; Conservative 19; Mismatches 16; Indels 1; Gaps 1;

QY 1 TNACSG-NAPABIDLRQMTVPIRMQCGCGSCWAFSGVAATESAYLAHRNOSLDLAE 59
DB 99 TYACINSVSLPSLDLRLSLRTVPIRMQCGCGSCWAFSGVASTESAYLAHRNOSLDLAE 158

QY 60 QELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFISNYCOI 119
DB 159 QELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRYGLKNYCOI 218

QY 120 YPPNANKIREALAQTHSAIAVIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSN 179
DB 219 SPDSNKRQALQTHTAVAVIIGIKDLNAPFRHYDGRITIMQHDNGYQPNYHVNIVGYSN 278

QY 180 AQGVYWIVRNSWDTNMGDNGYGYFAANIDLMIEEYPYVVL 222
DB 279 TQGVYWIVRNSWDTNMGDNGYGYFAANINLMIEEYPYVVL 321

RESULT 3
MMAL DERFA
ID MMAL_DERFA STANDARD; PRT; 321 AA.
AC P16311;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Major mite fecal allergen Der f 1 precursor (EC 3.4.22.-) (Der f I).
GN Name=DERf1;
OS Dermatophagoides farinae (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcophormes; Astigmata; Psoroptidia; Analgoidea;
OC Pyroglyphidae; Dermatophagoides.
OX NCBI_TaxID=6954;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91215493; PubMed=2021874;
RA Dilworth R.J.; Chua K.Y.; Thomas W.R.;
RT "Sequence analysis of cDNA coding for a major house dust mite
RT allergen, Der f I."
RL Clin. Exp. Allergy 21:25-32(1991).
RN [2]
RP SEQUENCE OF 98-309 FROM N.A.
RA Kent N.; Hill M.R.; Keen J.N.; Holland P.W.; Hart B.J.;
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 99-128.
RX MEDLINE=88229138; PubMed=3372999;
RA Lind P.; Hansen O.C.; Horn N.;

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RT "The binding of mouse hybridoma and human IgE antibodies to the major
RT fecal allergen, Der p 1, of Dermatophagoides pteronyssinus. Relative
RT binding site location and species specificity studied by solid-phase
RT inhibition assays with radiolabeled antigen.";
RL J. Immunol. 140:4256-4262(1988).
CC -I- FUNCTION: Thiol protease that hydrolyzes proteins, with a
CC preference for phe or basic residues.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- ALLERGEN: Causes an allergic reaction in human. Common symptoms of
CC mite allergy are bronchial asthma, allergic rhinitis and
CC conjunctivitis.
CC -I- SIMILARITY: Belongs to the peptidase C1 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X65196; CAA46316.1; -.
CC PIR; A27634; A27634.
CC HSP; P53634; IK3B.
CC MEROPS; C01.073; -.
DR InterPro; IPR000169; Pept_cys_actsite.
DR InterPro; IPR000668; Peptidase_C1.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPA1N.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept C1; 1.
DR PROSITE; PS00640; THIOI_PROTEASE ASN; 1.
DR PROSITE; PS00139; THIOI_PROTEASE CYS; 1.
DR PROSITE; PS00639; THIOI_PROTEASE HIS; 1.
KW Allergen; Direct protein sequencing; Glycoprotein; Hydrolase; Signal;
KW Thiol protease; Zymogen.
FT SIGNAL 1 18 Potential.
FT PROPEP 19 98 Activation peptide.
FT CHAIN 99 321 Major mite fecal allergen Der f 1.
FT ACT_SITE 133 133 By similarity.
FT ACT_SITE 269 269 By similarity.
FT ACT_SITE 288 288 By similarity.
FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).
FT DISULFID 130 170 By similarity.
FT DISULFID 164 202 By similarity.
FT CONFLICT 201 201 R -> Q (in Ref. 2).
FT CONFLICT 282 282 D -> V (in Ref. 2).
SQ SEQUENCE 321 AA; 36435 MW; 04523E54EBB476E CRC64;

Query Match 82.7%; Score 997.5; DB 1; Length 321;
Best Local Similarity 81.2%; Pred. No. 3.3e-81;
Matches 181; Conservative 18; Mismatches 23; Indels 1; Gaps 1;

QY 1 TNACSG-NAPABIDLRQMTVPIRMQCGCGSCWAFSGVAATESAYLAHRNOSLDLAE 59
DB 99 TSACRINSVNPSELDLRLSLRTVPIRMQCGCGSCWAFSGVAATESAYLAHRNOSLDLAE 158

QY 60 QELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFISNYCOI 119
DB 159 QELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRYGLKNYCOI 218

QY 120 YPPNANKIREALAQTHSAIAVIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSN 179
DB 219 YPPDVKQIREALQTHTAVAVIIGIKDLNAPFRHYDGRITIMQHDNGYQPNYHVNIVGYSN 278

QY 180 AQGVYWIVRNSWDTNMGDNGYGYFAANIDLMIEEYPYVVL 222
DB 279 TQGVYWIVRNSWDTNMGDNGYGYFAANINLMIEEYPYVVL 321

RESULT 4
Q9GYO

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ID Q9GYX0 PRELIMINARY; PRT; 210 AA.
AC Q9GYX0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Allergen Der f1 (Fragment).
OS Dermatophagoides farinae (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcotiformes; Astigmata; Psoroptidia; Analgoidea;
OC Pyroglyphidae; Dermatophagoides.
OX NCBI_TaxID=6954;
RN [1]
RP SEQUENCE FROM N.A.
RA Hao M.Q., Xu J., Zhong N.S.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family C1.
DR EMBL; A285763; AAG00520.1; -.
DR PIR; A27634; A27634.
DR HSSP; P80067; 1JQP.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; Pept_cys_acsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR SMART; SM00645; Pept C1; 1.
DR PROSITE; PS00640; THIOL_PROTEASE ASN; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
KW Hydrolase; Protease; Thiol protease.
FT NON_TER 1
FT NON_TER 210
SQ SEQUENCE 210 AA; 23548 MW; BA08029D642EB90 CRC64;

Query Match 78.3%; Score 944.5; DB 2; Length 210;
Best Local Similarity 81.4%; Pred. No. 1.1e-76;
Matches 171; Conservative 16; Mismatches 22; Indels 1; Gaps 1;

QY 2 NACSING-NAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
DB 1 SACRINSVNPSELDRLSRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLSEQ 60

QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRPNRAQFGISNYCQIY 120
DB 61 ELVDCASQHGCHGDTIPRGIEYIQNGVVEERSYPVAREQSCRPNRAQFGISNYCQIY 120

QY 121 PPNANKIREALQTHAIAVIIGIKDLAPRHYDGRITIQRDNGYQPNYHVNIVGYSNA 180
DB 121 PPDVKQIREALTQTHAIAVIIGIKDLAPRQHYDGRITIIQHDNGYQPNYHVNIVGYGST 180

QY 181 QGVYDYMVRNSWDTNMGDNGYGYFAANIDL 210
DB 181 QGVYDYMVRNSWDTTWGDSGYGYFQAGNNL 210

RESULT 5
Q95X05 PRELIMINARY; PRT; 146 AA.
AC Q95X05;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cysteine proteinase (Fragment).
GN Names=CPW2;
OS Dermatophagoides farinae (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcotiformes; Astigmata; Psoroptidia; Analgoidea;
OC Pyroglyphidae; Dermatophagoides.
OX NCBI_TaxID=6954;
RN [1]
RP SEQUENCE FROM N.A.
RA Park H., Park S.Y., Kim K.Y., Park S.K., Yun H.C.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF194431; AAL14424.1; -.
DR HSSP; P43235; 1BY8.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000668; Peptidase_C1.
DR Pfam; PF00112; Peptidase_C1; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16852 MW; BB304800946D4047 CRC64;

Query Match 50.3%; Score 607; DB 2; Length 146;
Best Local Similarity 84.2%; Pred. No. 1.5e-46;
Matches 112; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 39 GVAATESAYLAHRNOSLDLAEQELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVA 98
DB 1 GVAATESAYLAHRNOSLDLSEQELVDCASQHGCHGDTIPRGIEYIQNGVVEERSYPVA 60

QY 99 RQSCRRPNRAQFGISNYCQIYPPNANKIREALQTHAIAVIIGIKDLDAFRHYDGRIT 158
DB 61 RQSCRRPNRAQFGISNYCQIYPPDVVKQIREALTQTHAIAVIIGIKDLRAFOHYDGRIT 120

QY 159 IORDNGYQPNYHA 171
DB 121 IQHDNGYQPNYHA 133

RESULT 6
Q819P1 PRELIMINARY; PRT; 263 AA.
AC Q819P1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Derp1 antigen (Fragment).
OS Psoroptes ovis (Sheep scab mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcotiformes; Astigmata; Psoroptidia; Sarcotoides;
OC Psoroptidae; Psoroptes.
OX NCBI_TaxID=83912;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22294898; PubMed=12406195;
RA Lee A.J., Machell J., Van Den Broek A.H.M., Nisbet A.J.,
RA Miller H.R.P., Isaac R.E., Huntley J.F.;
RT Identification of an antigen from the sheep scab mite, Psoroptes
RT ovis, homologous with house dust mite group 1 allergens.;
RL Parasite Immunol. 24:413-422(2002).
DR EMBL; AF495854; AAO14671.1; -.
DR HSSP; P14080; 1YAL.
DR MEROPS; C01.073; -.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; Pept_cys_acsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept_C1; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
FT NON_TER 1
FT NON_TER 263
SQ SEQUENCE 263 AA; 29576 MW; BF6DD21006DAB5B0 CRC64;

Query Match 49.0%; Score 591.5; DB 2; Length 263;
Best Local Similarity 64.4%; Pred. No. 7.2e-45;
Matches 112; Conservative 22; Mismatches 39; Indels 1; Gaps 1;

QY 3 ACSING-NAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 61
DB 90 ACOIGAVNIPNEIDLRAIGVTKIKNQVACGSCWAFSGVATVESVLYSDNVSLDSEQ 149

QY 62 LVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRPNRAQFGISNYCQIYP 121
DB 62 LVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRPNRAQFGISNYCQIYP 121
```

Query Match	36.2%;	Score 437;	DB 2;	Length 133;
Best Local Similarity	61.4%;	Pred. No. 2.4e-31;		
Matches	81;	Conservative	17;	Mismatches 34; Indels 0; Gaps 3

Qy	31	CGSCWAFSGVAATESAYLAHRNQSLLDAEQBLVDCASQHGCHGDTIPRGIEYIOHNGVQ	90
Db	1	CGSCWAFGVAAVESAYLAFRNQINLAEQBLVDCAAARRGCHGDTIPRLGDIYQNGIVE	60
Qy	91	ESYYRYVAREQSCRRPNAQREGISNYCOIYPPNANKIREALQTHSAIAVIIGIKDLDAF	150
Db	61	EQAYEVNARENNCPENPRHSIQYCOIDHSNVELIKTALDKYKSAAVIINIHNAF	120
Qy	151	RHYDRTIIORD	162
Db	121	RHYDGSYVITTD	132

RESULT 9				
Q7M431		PRELIMINARY;	PRT;	94 AA.
AC	Q7M431;			
DT	01-MAR-2004	(TREMBlrel. 26, Created)		
DT	01-MAR-2004	(TREMBlrel. 26, Last sequence update)		
DE	01-MAR-2004	(TREMBlrel. 26, Last annotation update)		
OS	Major fecal allergen Der p I (Fragments).			
OC	Dermatophagoides pteronyssinus (House-dust mite).			
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;			
OC	Acariiformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;			
OC	Pyroglyphidae; Dermatophagoides.			
OX	NCBI_TaxId=6956;			
RP	[1]			
RP	SEQUENCE.			
RX	MEDLINE=89098855; PubMed=2911558;			
RA	Simpson R.J., Nice E.C., Moritz R.L., Stewart G.A.;			
RT	"Structural studies on the allergen Der p1 from the house dust mite			
RT	Dermatophagoides pteronyssinus: similarity with cysteine			
RT	proteinases."			
RL	Protein Seq. Data Anal. 2:17-21(1989).			
DR	PIR; S03380; S03380.			
DR	GO; GO:0008234; P:cysteine-type peptidase activity; IEA.			
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR000668; Peptidase_C1.			
DR	ProDom; PD000158; Peptidase_C1; 1.			
FT	NON TER	1		
FT	NON TER	94		
FT	NON TER	94		
SQ	SEQUENCE	94 AA; 10327 MW; 9BF744165C6428A8	CRC64;	

Query Match	32.3%;	Score 389.5;	DB 2;	Length 94;
Best Local Similarity	48.6%;	Pred. No. 2.9e-27;		
Matches	88;	Conservative	0;	Mismatches 4; Indels 89; Gaps 4

Qy	1	TNACSIGNAPAEIDLQRMRTVTPIR--MQGCGSCWAFSGVAATESAYLAHRNQSLLDA	58	
Db	1	TNACSIGNAPAEIDLQRMRTVTPIRQMCGCGSCXXAFSGVA-----	43	
Qy	59	EQELVDCASQHGCHGDTIPRGIEYIOHNGVQESYRYVAREQSCRRPNAQREGISNYCO	118	
Db	44	-----GIEYIOHNGVQESYY-----RFGISNYCO	68	
Qy	119	IYPPNANKIREALQTHSAIAVIIGIKDLDAFRHYDGTITIQRDNGYQPNYHANNVIGYS	178	
Db	69	IYPPNANK-----DNGYQPNYXAVNIVGYX	93	
Qy	179	N 179		
Db	94	N 94		

RESULT 10				
Q95P04		PRELIMINARY;	PRT;	221 AA.
ID	Q95P04			
AC	Q95P04;			
DT	01-DEC-2001	(TREMBlrel. 19, Created)		


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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cysteine protease (Fragment).
OS Blomia tropicalis (Mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptiformes; Astigmata; Glyciphagoidea;
OC Echinypodidae; Blomia.
OX NCBI_TaxID=40697;
RN [1]
RN SEQUENCE FROM N.A.
RA Mora C.I., Diaz A.M., Montealegre F., Flores I.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF277840; AAK58415.1; -.
DR HSSP; P53634; 1K3B.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000668; Peptidase_C1.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR SMART; SM00645; Pept C1; 1.
DR PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; UNKNOWN_1.
KW Protease.
FT NON_TER
FT CHAIN
SQ SEQUENCE 221 AA; 25126 MW; 272845E5A53F2900 CRC64;

Query Match 31.7%; Score 382; DB 2; Length 221;
Best Local Similarity 38.4%; Pred. No. 3.7e-26;
Matches 86; Conservative 35; Mismatches 77; Indels 26; Gaps 8;

QY 11 PAEIDLQRMRTVTPIRMQGGCGSWAFSGVAATESAYLAHRNQSLLAEQELVDCASQ-- 68
Db 2 PANFDWRQKTHVNPINRQGGCGSWAFSGVAATESAYLAHRNQSLLAEQELVDCASQ 61

QY 69 -----HGCHGDTIPRGIEYIQHNGVQVESYRYVAREQSCRPNNAQ--RFGISNYCQIY 120
Db 62 DPTYKCHGCGSGMSPEAFKYMKGKGLLESHYFYKMKLQC-QANARGTRYHVSSY---- 116

QY 121 PPNANKIREALQTHSAI-----AVIGIKDLDA-FRHYDGRTHIQRDNGVQPNY--HAVN 173
Db 117 --NSLRYRAGDQBIQAIIMHNPVWYVYHGTAEHFNRL--RKGLRGAGYNDQAIDHAVV 172

QY 174 IVGYSNAQGVYVIVNSWDNMGNGYGYFAANIDLMMIEEYP 217
Db 173 LVGWTQNGIDYVIVTSMGTQWDAGYGFVERHNSLGINNP 216

RESULT 11
Q7SXQ7 PRELIMINARY; PRT; 333 AA.
AC Q7SXQ7
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cathespin.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Typhlosole;
RX MEDLINE=22871689; PubMed=14507309;
RA Unuk-Ool T.S., Takezaki N., Kuroda N., Figueroa F., Sato A.,
RA Samonte I.E., Mayer W.E., Klein J.;
RT "Phylogeny of antigen-processing enzymes: cathepsins of a
RT cephalochordate, an agnathan and a bony fish.";
RL Scand. J. Immunol. 58:436-448(2003).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Typhlosole;

RA Unuk-ool T.S., Takezaki N., Kuroda N., Figueroa F., Sato A.,
RA Samonte I.E., Mayer W.E., Klein J.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF333299; AAO01146.1; -.
DR HSSP; P25774; IGLO.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; Pept_cys_acsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept C1; 1.
DR PROSITE; PS00640; THIOI_PROTEASE ASN; 1.
DR PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.
KW Hydrolase; Protease; Thiol protease.
SQ SEQUENCE 333 AA; 37500 MW; 0B0D129A748B099A CRC64;

Query Match 28.3%; Score 341.5; DB 2; Length 333;
Best Local Similarity 36.0%; Pred. No. 2.6e-22;
Matches 80; Conservative 36; Mismatches 91; Indels 15; Gaps 9;

QY 9 NPAEIDLQRMRTVTPIRMQGGCGSWAFSGVAATESAYLAHRNQSLLAEQELVDCASQ 68
Db 116 NLPEQVDWRLKGYVTPVKEQGLCGSSWAFSGVATGNTLSLSEQLVDCSTKS 175

QY 69 H---GCHGDTIPRGIEY-IQHNGVQVESYRYVAREQSCR-RPNAQRFGISNYCQIYPPN 123
Db 176 YVNGGCGGRSERALQYIIDNGIDSELSYPYEHADGCKRFPANVATKCSSY-QFVEPS 234

QY 124 ANK--IREALQTHSAIAVIGIKDLDAFRHYDGRTHIQRDNGVQPNYHAVNIVGYSNAQ 181
Db 235 SNEEVLQRQAVSY-GPIATAMN-ADLDTFKHGLFNEPSCDKSPN-HAMLVVVGSL 291

QY 182 GVDYVTVRNSWDNMGNGYGYFAANIDLMMIEEYPYV 219
Db 292 GNDFWIVKNSWGEDWGEKGYIYWRKNQCGIASIGIYPII 333

RESULT 12
Q6ZHP9 PRELIMINARY; PRT; 366 AA.
AC Q6ZHP9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative cysteine proteinase.
GN Names=OJ1191.G08.11;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RN SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC
RT clone:OJ1191.G08.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family C1.
DR EMBL; AF004047; BAD03165.1; -.
DR HSSP; P00785; IAC.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; Pept_cys_acsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept_C1; 1.
DR PROSITE; PS00640; THIOI_PROTEASE ASN; 1.
DR PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.
KW Hydrolase; Protease; Thiol protease.
SQ SEQUENCE 366 AA; 40600 MW; 89529D2315608C4C CRC64;

Query Match 27.6%; Score 332.5; DB 2; Length 366;

```

Best Local Similarity 35.7%; Pred. No. 1.9e-21;
Matches 79; Conservative 34; Mismatches 91; Indels 17; Gaps 7;

Qy 9 NAPAEDLRQMTVTPIRMQGGCGSCWAFSAVAATESAYLAHRNQSLLDLAEQELVDCAS- 67
Db 142 NLPWAVDRKKGATVPKNGQCGSCWAFSAVAATEGINQIVTGKLSLSEQELMDCDNT 201
Qy 68 -QHCHGDTIPRGIEYIQHNVGVQESYRYRYVAREQSCR--RPNARFGISNYCQIYPPN 123
Db 202 FNHCGRGLMDFAFAYTMGNQIYTEEDYPYLMEEGYCREKQPHSKVITITGYEDVPANS 261
Qy 124 ANKIREALQTHSAIAVIGIKLDAFRHYDGRITIIQORDNGYQYHNAVITGVSNAGV 183
Db 262 ETSLLKALAHQPVSVGTAAGSRD---FQYKRG-GFDGEGCIQPD-HALTAVGYGSYYGQ 316
Qy 184 DYIWMKSNWGNWGEQGYFRIRRGTRGPEGVCDIYKIASYP 217
Db 317 DYIWMKSNWGNWGEQGYFRIRRGTRGPEGVCDIYKIASYP 357

RESULT 13

Q9ZQH7
ID Q9ZQH7 PRELIMINARY; PRT; 348 AA.
AC Q9ZQH7
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cysteine proteinase.
GN Name=At2g2420;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
RA Davis R.W., Ecker J.R., Theologis A.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family C1.
DR EMBL; AC006232; AAD15594.1; -
DR EMBL; AY064033; AAL36389.1; -
DR EMBL; AY096388; AAM20029.1; -
DR PIR; F84672; F84672.
DR HSP; P53634; IK3B.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000668; Peptidase_C1.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept_C1; 1.
DR PROSITE; PS00640; THIOI_PROTEASE ASN; 1.
DR PROSITE; PS00139; THIOI_PROTEASE CYS; 1.
DR PROSITE; PS00639; THIOI_PROTEASE HIS; UNKNOWN 1.
KW Hydrolase; Protease; Thiol protease.
SQ SEQUENCE 348 AA; 38738 MW; EB86ABEC2B553E76 CRC64;

Query Match 27.5%; Score 332; DB 2; Length 348;
Best Local Similarity 36.2%; Pred. No. 1.9e-21;
Matches 84; Conservative 32; Mismatches 86; Indels 30; Gaps 11;

Qy 5 SINGNAPAEIDLRQMTVTPIRMQGGCGSCWAFSAVAATESAYLAHRNQSLLDLAEQELVD 64
Db 126 SDNGES---MDWRQEGAVTPVKYQRCGCGWAFSAVAAREGITKITKGELVSLSEQQLLD 182
Qy 65 CASQH--GCHGDTIPRGIEY-IQHNGVQESYRYRYVAREQSCRPN- ----QRFGISNY 116
Db 183 CDRDYNQCGGIMSKAFVILKNGITTEDNTPYQESQTCSSSTLSSSFRAATISGY 242
Qy 117 CQYPPNANKIREALQTHSAIAVIGIKLDAFRHYDGRITIIQORDNGY--QPNYHAVN 173
Db 243 -ETVPMNN---EEALLQAVSQPVSVGIEGTGAFRHYSGGVF---NGEGCTDLHHAVT 294
Qy 174 IVGYS-NAQGVYVIVNSMDTWGDNQGYVFAANID- ----LMMIEEYP 217
Db 295 IVGYMSEEGTKYVWVKNWGETWNGYWRKRDVDAPOGMCGLAILAFYP 346

RESULT 14

Q717S6
ID Q717S6 PRELIMINARY; PRT; 326 AA.
AC Q717S6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative gut cathepsin L-like cysteine protease.
GN Name=CPA15;
OS Callosobruchus maculatus (cowpea weevil).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Phytophaga; Chrysomeloidea; Chrysomelidae; Bruchinae; Bruchini;
OC Callosobruchus.
OX NCBI_TaxID=64391;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhu-Salzman K., Ahn J.-E., Koiba H., Salzman R.A.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family C1.
DR EMBL; AF544838; AAQ11969.1; -
DR HSP; P43235; IAYU.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000668; Peptidase_C1.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept_C1; 1.
DR PROSITE; PS00640; THIOI_PROTEASE ASN; 1.
DR PROSITE; PS00139; THIOI_PROTEASE CYS; 1.
DR PROSITE; PS00639; THIOI_PROTEASE HIS; 1.
KW Hydrolase; Protease; Thiol protease.
SQ SEQUENCE 326 AA; 36653 MW; A9265E018FFD2A8D CRC64;

Query Match 27.4%; Score 331; DB 2; Length 326;
Best Local Similarity 32.7%; Pred. No. 2.2e-21;
Matches 71; Conservative 38; Mismatches 94; Indels 14; Gaps 6;

Search completed: May 19, 2005, 17:22:44
Job time : 62 secs

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QY 14 IDLRQMTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAQELVDCASQ----H 69
Db 116 VDWREGAVTPVKDQANCGSCWAFSAVGALEGQFFKNGTGLVLSAQELVDCATEDYGN 175
QY 70 GCHGDTIPRGIEYIQHNGVQVESYRYVAREQSCRPNQAFGISNYCQIYPNPANKIRE 129
Db 176 GCKGGLMGQAFDFVQDEGIQTEESYPVEGRSSCKSGEYVTKVY--VFPLDEQEMAR 233
QY 130 ALAQTHSAIAVIIGIKDLDAPRHYDRTIQR---DNGQPNTNHNIVGYSNAQGVY 186
Db 234 TVA-AKGPVAVATEASQLS---FYDKGIVDRCRCSNKREDLNHGLVWVGSGENGVDY 289
QY 187 IVNSDNTNWDNGYGYFAANIDLMIEEY-PYVVIL 222
Db 290 IVKNSGADMGEGYFLKDKVAKAGIGYNNYPILL 326
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RESULT 15

```
Q6E7B4 PRELIMINARY; PRT; 393 AA.
AC Q6E7B4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Cathepsin L-like cysteine proteinase.
GN Name=CPL-4;
OS Brugia malayi (Filarial nematode worm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Brugia.
OX NCBI_TaxID=6279;
RN [1]
RP SEQUENCE FROM N.A.
RA Guillian D.B., Hong X., McKerrow J.H., Blaxter M.L., Oksav Y., Liu J.,
RA Ghedin E., Lustigman S.;
RT "A gene family of cathepsin L-like proteases of filarial nematodes are
RT associated with larval molting and cuticle and eggshell remodeling.";
RL Mol. Biochem. Parasitol. 136:227-242(2004).
CC -|- SIMILARITY: Belongs to peptidase family C1.
DR EMBL; AY533166; AAU07057.1; -.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000668; Peptidase C1.
DR InterPro; IPR000169; Pept. cys AcSite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept C1; 1.
DR PROSITE; PS00640; THIOI_PROTEASE ASN; 1.
DR PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.
KW Hydrolase; Protease; Thiol protease.
SQ SEQUENCE 393 AA; 44527 MW; C0A34546595B1E93 CRC64;
```

```
Query Match 27.4%; Score 330.5; DB 2; Length 393;
Best Local Similarity 37.9%; Pred. No. 3.1e-21;
Matches 77; Conservative 32; Mismatches 83; Indels 11; Gaps 7;
QY 11 PAEIDLQMTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAQELVDCASQ---S 67
Db 181 PDLVWRRTKGAIVFVRNQGCGCYAFATAALEAYHKQMTGRLLDLSQNIIVDCTWDLG 240
QY 68 QHCGDGTIPRGIEYIQHNGVQVESYRYVAREQSCR-RPNAQRFGISNYCQIYPNPANK 126
Db 241 NKCGNGYMTAFQYASRYGIAMESYPYVGTQRQRWQNIIVTDTNGFNEIQPDELA 300
QY 127 IREALAQTSHAIAVIIGIKDLDAPRHY-DGRTIIQRDNGQPNYHVNIVGYSNAQGV-D 184
Db 301 LKHAVAKRGPVVVGISGSK--RSFRFYKDG--VYSEGNCGRPD-HAVLVVGYGTDRTSYG 355
QY 185 YWIVRNSDNTNWDNGYGYFAAN 207
Db 356 YWIVRNSDNTNWDNGYGYFAAN 378
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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:12:26 ; Search time 164 Seconds
(without alignments)
523.541 Million cell updates/sec

Title: US-09-867-159a-2

Perfect score: 1206

Sequence: 1 TNACSSINGNAPAEIDLQMR.....YFAANIDLMIEPPYVIL 222

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1206	100.0	222	5	AAO20568 Cysteine
2	1206	100.0	222	5	ABB98533 Cysteine
3	1206	100.0	245	2	AAR22433 Der p I a
4	1206	100.0	245	2	AAR39359 Dermatoph
5	1206	100.0	245	2	AAR51727 Der p I.
6	1206	100.0	245	2	AAR47063 Protein a
7	1206	100.0	245	2	AAR66545 Der p I a
8	1206	100.0	245	2	AAW71908 Dermatoph
9	1206	100.0	245	2	AAW50356 Dermatoph
10	1206	100.0	245	4	AAU18959 House dus
11	1206	100.0	245	5	ABG71812 European
12	1206	100.0	320	2	AAR49920 Protein a
13	1203	99.8	222	4	AAU07748 House dus
14	1200	99.5	222	4	AAU07748 House dus
15	1200	99.5	302	4	AAU07748 House dus
16	1200	99.5	302	5	AAU07748 House dus
17	1200	99.5	302	8	AAU07748 House dus
18	1199	99.4	362	8	AAU07748 House dus
19	1196	99.2	222	4	AAU07748 House dus
20	1196	99.2	222	5	AAU07748 House dus
21	1196	99.2	222	8	AAU07748 House dus
22	1196	99.2	222	8	AAU07748 House dus
23	1196	99.2	223	4	AAU07748 House dus
24	1196	99.2	223	4	AAU07748 House dus
25	1196	99.2	282	8	ADL27398 Polypepti

26	1196	99.2	302	4	AAU07748 House dus
27	1196	99.2	302	4	AAU07748 House dus
28	1196	99.2	302	6	AAU07748 House dus
29	1196	99.2	302	8	AAU07748 House dus
30	1196	99.2	303	4	AAU07748 House dus
31	1196	99.2	320	2	AAU07748 House dus
32	1196	99.2	320	2	AAU07748 House dus
33	1196	99.2	320	4	AAU07748 House dus
34	1196	99.2	320	6	AAU07748 House dus
35	1196	99.2	320	6	AAU07748 House dus
36	1196	99.2	320	7	AAU07748 House dus
37	1196	99.2	320	7	AAU07748 House dus
38	1196	99.2	320	8	AAU07748 House dus
39	1196	99.2	320	8	AAU07748 House dus
40	1196	99.2	320	8	AAU07748 House dus
41	1196	99.2	320	8	AAU07748 House dus
42	1195	99.1	339	2	AAU07748 House dus
43	1191	98.8	320	6	AAU07748 House dus
44	1191	98.8	343	2	AAU07748 House dus
45	1189	98.6	222	4	AAU07748 House dus

ALIGNMENTS

RESULT 1
AAO20568
ID AAO20568 standard; protein; 222 AA.
XX
AC AAO20568;
XX
DT 02-JAN-2003 (first entry)
XX
DE Cysteine protease protein.
XX
KW Antiallergic; antiinflammatory; antiasthmatic; dermatological; allergen;
KW anti-histamine; histamine synthesis inhibitor; allergic hypersensitivity;
KW allergic asthma; allergic rhinitis; cysteine protease protein; enzyme;
KW atopic eczema.
XX
OS Dermatophagoides pteronyssinus.
XX
FH Key Location/Qualifiers
FT Misc-difference 105
FT /note= "Encoded by ACC"
XX
PN WO200278736-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-FR001098.
XX
PR 30-MAR-2001; 2001FR-00004370.
PR 03-MAY-2001; 2001FR-00005929.
PR 29-MAY-2001; 2001US-00867159.
XX
PA (ANTI-) ANTIALIS SARL.
XX
PI Loria E, Terrasse G, Trehin Y;
XX
DR WPI; 2002-750636/81.
DR N-PSDB; AAL41281.
XX
PT Antiallergic compositions containing an anti-histamine, a histamine
PT synthesis inhibitor, and optionally an allergen or nucleic acid coding
PT for the allergen.
XX
PS Claim 13; Page 30-31; 32pp; French.
XX
CC The invention relates to antiallergic compositions containing an anti-
CC histamine, a histamine synthesis inhibitor, and optionally an allergen or
CC isolated nucleic acid molecule that has at least one polynucleotide
CC sequence coding for the allergen, together with a pharmaceutical carrier.

CC The pharmaceutical composition of the invention is useful as a non-specific anti-allergic treatment, and also useful in the treatment of allergic hypersensitivity, allergic asthma, allergic rhinitis, and allergic atopic eczema. This sequence represents the cysteine protease protein relating to the anti-allergic compositions of the invention

XX
XX
SQ Sequence 222 AA;

Query Match 100.0%; Score 1206; DB 5; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.7e-127;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNACSLNGNAPAEIDLRQMRVTPTIRMOGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
DB 1 TNACSLNGNAPAEIDLRQMRVTPTIRMOGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60

QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQVESYRYVAREQSCRRPNAQRFGISNYCQIY 120
DB 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQVESYRYVAREQSCRRPNAQRFGISNYCQIY 120

QY 121 PPNAKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQRDNGYQPNYHAVNIVGYSNA 180
DB 121 PPNAKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQRDNGYQPNYHAVNIVGYSNA 180

QY 181 QGVYDWIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVVIL 222
DB 181 QGVYDWIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVVIL 222

RESULT 2
ABB98533
ID ABB98533 standard; protein; 222 AA.
XX
AC ABB98533;
XX
DT 13-DEC-2002 (first entry)
XX
DE Cysteine protease.
XX
KW Antiallergic; antiasthmatic; antiinflammatory; dermatological; immunotherapy; allergen; allergic hypersensitivity reaction;
KW allergic asthma; allergic rhinitis; allergic atopic eczema;
KW cysteine protease.
XX
OS Dermatophagoides pteronyssinus.
XX
FH Key Location/Qualifiers
FT Misc-difference 105
FT /note= "Encoded by CCA"
XX
PN FR2822709-A1.
XX
XX
PD 04-OCT-2002.
XX
PF 03-MAY-2001; 2001FR-00005929.
XX
PR 30-MAR-2001; 2001FR-00004370.
XX
PA (ANTI-) ANTIALIS SARL.
XX
XX Loria E, Terrasse G, Trehin Y;
XX WPI; 2002-735037/80.
DR N-PSDB; ABQ80833.
XX
XX Antiallergic composition, useful for preventing and treating e.g. asthma, rhinitis or eczema, containing at least two of allergen, antihistamine and histamine synthesis inhibitor.
XX
PS Claim 7; Page 27-28; 33pp; French.
XX
CC The present invention relates to an anti-allergic pharmaceutical

CC composition (I) comprising a pharmaceutical carrier containing an active agent combination of at least two of: an allergen; an antihistamine; and a histamine synthesis inhibitor. (I) is used for treating or preventing allergic hypersensitivity reactions, especially allergic asthma, allergic rhinitis or allergic atopic eczema, in babies, children or adults. The present sequence is cysteine protease from Dermatophagoides pteronyssinus, which was used as an allergen in the invention

XX
SQ Sequence 222 AA;

Query Match 100.0%; Score 1206; DB 5; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.7e-127;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNACSLNGNAPAEIDLRQMRVTPTIRMOGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
DB 1 TNACSLNGNAPAEIDLRQMRVTPTIRMOGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60

QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQVESYRYVAREQSCRRPNAQRFGISNYCQIY 120
DB 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQVESYRYVAREQSCRRPNAQRFGISNYCQIY 120

QY 121 PPNAKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQRDNGYQPNYHAVNIVGYSNA 180
DB 121 PPNAKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQRDNGYQPNYHAVNIVGYSNA 180

QY 181 QGVYDWIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVVIL 222
DB 181 QGVYDWIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVVIL 222

RESULT 3
AAR22433
ID AAR22433 standard; protein; 245 AA.
XX
AC AAR22433;
XX
DT 27-AUG-2003 (revised)
DT 04-AUG-1992 (first entry)
XX
DE Der p I allergen.
XX
KW House dust mite; desensitisation therapy; sensitivity.
XX
OS Dermatophagoides pteronyssinus.
XX
FH Key Location/Qualifiers
FT Cleavage-site 7..8
FT /note= "signal peptide cleavage"
FT Modified-site 68..70
FT /note= "N-glycosylation site"
XX
PN WO9204445-A.
XX
PD 19-MAR-1992.
XX
PF 10-SEP-1991; 91WO-AU000417.
XX
PR 11-SEP-1990; 90US-00580655.
XX
PA (WAUR-) WEST AUST RES INST.
XX
XX Thomas WR, Chua KY;
XX WPI; 1992-114353/14.
DR N-PSDB; AAQ23373.
XX
XX DNA encoding allergens of house dust mite Dermatophagoides - and isolated protein allergens and peptide(s) useful in treating and detecting sensitivity to mites, esp. D. farinae.
XX
PS Claim 14; Fig 7; 53pp; English.
XX

CC The protein sequence was deduced from the cDNA sequence obtd. by
 CC screening a dermatophagoides cDNA library with two probes comprising the
 CC Der p 1 cDNA BamHI fragments 1-348 and 349-857. The protein allergen is
 CC used as a diagnostic reagent in detecting and treating sensitivity to
 CC house dust mites and in desensitisation therapy. See also AAR22431,2.
 CC (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 245 AA;

Query Match 100.0%; Score 1206; DB 2; Length 245;
 Best Local Similarity 100.0%; Pred. No. 3.1e-127;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNACSSINGNAPAEIDLQMTVTPIRMQGGCGSWAFSGVAATESAYLAHRNQSLDLAEQ 60
 DB 24 TNACSSINGNAPAEIDLQMTVTPIRMQGGCGSWAFSGVAATESAYLAHRNQSLDLAEQ 83
 QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRPNARPGISNYCQIY 120
 DB 84 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRPNARPGISNYCQIY 143
 QY 121 PPNAKIREALAOQTHSAIAVIIGIKOLDAPFRHYDGRITIIQDNGYQPNYHVNIVGYSNA 180
 DB 144 PPNAKIREALAOQTHSAIAVIIGIKOLDAPFRHYDGRITIIQDNGYQPNYHVNIVGYSNA 203
 QY 181 QGVDDYWIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 222
 DB 204 QGVDDYWIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 245

RESULT 4
 AAR39359
 ID AAR39359 standard; protein; 245 AA.

AC AAR39359;
 XX
 DT 25-MAR-2003 (revised)
 DT 12-AUG-1993 (first entry)
 XX
 DE Dermatophagoides pteronyssinus Dep p1.
 XX
 KW T cell epitope; house dust mite; allergy; soluble; allergen.

XX Dermatophagoides pteronyssinus.

XX WO9308279-A1.

XX 29-APR-1993.

XX 15-OCT-1992; 92WO-US008637.

XX 16-OCT-1991; 91US-00777859.

PR 08-MAY-1992; 92US-00881396.

XX (IMMU-) IMMULOGIC PHARM CORP.

XX Garman RD, Greenstein JL, Kuo MC, Rogers BL;

XX WPI; 1993-152472/18.

DR N-PSDB; AAQ41211.

XX Isolated peptide(s) of dermatophagoides protein allergens - for diagnosis
 PT and treatment of sensitivity to house dust mite.

XX Disclosure; Page 47; 176pp; English.

XX The cDNA encoding Dermatophagoides pteronyssinus group I allergen Dep p1
 CC was obtd. in plasmid form as subclone from lambda gt11 (Chua et al., J.
 CC Exp. Med. 167: 175-182 (1988)). The cDNA was used to express a Dep p1
 CC allergen which was capable of raising an immune response when contacted
 CC with anti-Dep p1 antibodies. The protein was used to design a series of
 CC overlapping peptides synthesised by standard techniques to cover the
 CC whole Dermatophagoides pteronyssinus Dep p1 sequence. The T cell epitopes

CC of the protein were mapped by detection of the peptide's ability to
 CC stimulate T cell activity. The peptides may be used for diagnosis and
 CC treatment of sensitivity to house dust mite allergens. When administered
 CC to house dust mite sensitive individuals, the peptides are capable of
 CC modifying the allergic response to the allergens. The peptides may be
 CC modified for e.g. increasing solubility, enhancing therapeutic or
 CC preventive efficacy or stability. See also AAR34686-700, AAR36398-490 and
 CC AAR39360-2. (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 245 AA;

Query Match 100.0%; Score 1206; DB 2; Length 245;
 Best Local Similarity 100.0%; Pred. No. 3.1e-127;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNACSSINGNAPAEIDLQMTVTPIRMQGGCGSWAFSGVAATESAYLAHRNQSLDLAEQ 60
 DB 24 TNACSSINGNAPAEIDLQMTVTPIRMQGGCGSWAFSGVAATESAYLAHRNQSLDLAEQ 83
 QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRPNARPGISNYCQIY 120
 DB 84 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRPNARPGISNYCQIY 143
 QY 121 PPNAKIREALAOQTHSAIAVIIGIKOLDAPFRHYDGRITIIQDNGYQPNYHVNIVGYSNA 180
 DB 144 PPNAKIREALAOQTHSAIAVIIGIKOLDAPFRHYDGRITIIQDNGYQPNYHVNIVGYSNA 203
 QY 181 QGVDDYWIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 222
 DB 204 QGVDDYWIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 245

RESULT 5
 AAR51727
 ID AAR51727 standard; protein; 245 AA.

AC AAR51727;

DT 01-FEB-1995 (first entry)

DE Der p I.

XX Group I; protein allergen; house dust mite; D. pteronyssinus; Der p I;
 KW homology; D. farinae; Der f I; group II; Der p II; Der f II; T-cell;
 KW epitopes; fusion peptides; antigenic fragments; substitution; deletion;
 KW addition; chemical synthesis; chemical cleavage; recombinant techniques;
 KW allergic response; immunoglobulin E; IgE; immunotherapy; anaphylaxis;
 KW IgE-mediated responses; anergise; lymphokine secretion profile; modify;
 KW T cell subpopulations; unresponsive; immune response; tolerance.

XX Dermatophagoides pteronyssinus.

XX ZA9302677-A.

XX 26-JAN-1994.

XX 16-APR-1993; 93ZA-00002677.

XX 16-APR-1993; 93ZA-00002677.

XX (IMMU-) IMMULOGIC PHARM CORP.

XX Garman RD, Greenstein JL, Kuo M, Rogers BL;

XX WPI; 1994-126807/15.

DR N-PSDB; AAQ62308.

XX Isolated and/or modified peptides comprising T-cell epitopes - of major
 PT protein allergens of genus Dermatophagoides, used to treat or diagnose
 PT sensitivity to house dust mites.

XX Disclosure; Page 48-49; 154pp; English.

CC This sequence represents the group I protein allergen from the house dust
 CC mite *D. pteronyssinus*, Der p I. The Der p I protein shows high homology
 CC to the group I protein allergens derived from *D. farinae*, Der f I, having
 CC an identity of 81%. Fragments of these proteins, and the corresponding
 CC group II allergens, Der p II and Der f II, (see AAR51731-841) represent T
 CC - cell epitopes. Fusion peptides may be produced which comprise at least
 CC two or these antigenic fragments. Each region of these peptides may be
 CC derived from the same, or different, mite allergens. The antigenic
 CC fragments may be altered by substitution, deletion or addition to enhance
 CC their antigenicity. These peptides may be produced by chemical synthesis,
 CC chemical cleavage of the protein allergen or by recombinant techniques.
 CC These peptides, when administered to a house dust mite sensitive
 CC individual, are capable of modifying the allergic response of the
 CC individual to the allergen. These peptides do not bind to immuno- globulin
 CC E (IgE), or bind IgE to a lesser extent than the full length protein
 CC allergen. This reduces the major complications of standard immunotherapy,
 CC which are IgE-mediated responses such as anaphylaxis. Exposure of mite
 CC allergic patients to these peptides may tolerate or anergise appropriate
 CC T cell subpopulations such that they become unresponsive to mite
 CC allergens and do not participate in mounting an immune response upon
 CC exposure. Administration of the peptide may also modify the lymphokine
 CC secretion profile as compared with exposure to the naturally occurring
 CC mite protein allergen
 CC
 XX Sequence 245 AA;

Query Match 100.0%; Score 1206; DB 2; Length 245;
 Best Local Similarity 100.0%; Pred. No. 3.1e-127;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNACSSINGNAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
 DB 24 TNACSSINGNAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 83
 QY 61 ELVDCASQHGCHGDTTPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
 DB 84 ELVDCASQHGCHGDTTPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 143
 QY 121 PPANKIREALQTHSAIAVIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 180
 DB 144 PPANKIREALQTHSAIAVIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 203
 QY 181 QGVDDYWIVRNSWDTNWGDNGYGYFAANIDLMIMEEYPYVVIL 222
 DB 204 QGVDDYWIVRNSWDTNWGDNGYGYFAANIDLMIMEEYPYVVIL 245

RESULT 6
 AAR47063
 ID AAR47063 standard; protein; 245 AA.

XX AC AAR47063;
 XX DT 25-MAR-2003 (revised)
 XX DT 17-OCT-1994 (first entry)
 XX DE Protein allergen of Derp I.
 XX KW Der pI; House Dust Mite Allergen.
 XX OS Dermatophagoides pteronyssinus.
 XX FH Key Location/Qualifiers
 FT Protein 1..222 /label= Der pI preproenzyme
 FT Cleavage-site 9..111 /label= Cleavage site
 FT FT /note= "proenzyme remains"
 FT Cleavage-site 11..23 /label= cleavage site
 FT FT /note= "cleavage between pro-Der pI and pre-Der "

XX PN WO9405790-A1.

XX 17-MAR-1994.
 XX PD 10-SEP-1993; 93WO-US008518.
 XX PF 10-SEP-1992; 92US-00945288.
 XX PR (IMMU-) IMMULOGIC PHARM CORP.
 XX PA Thomas WR, Chua K;
 XX PI WPI; 1994-101195/12.
 XX DR N-PSDB; AAO58665.
 XX DR New protein allergens of house dust mite - used for diagnosing and
 XX PT treating sensitivity in an individual to house dust mite allergens.
 XX FT Example 1; Fig 1; 98pp; English.
 XX PS AAR47063 is a preproenzyme Der pI. The amino acid sequence preceding the
 XX CC mature protein sequence contains cleavage sites for the pre- and
 XX CC proenzyme forms, with residues 1-11 corresponding to a partial signal
 XX CC peptide sequence. The mature protein can be used to detect sensitivity in
 XX CC an individual to house dust mite and to reduce the sensitivity of the
 XX CC individual. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 245 AA;

Query Match 100.0%; Score 1206; DB 2; Length 245;
 Best Local Similarity 100.0%; Pred. No. 3.1e-127;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNACSSINGNAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
 DB 24 TNACSSINGNAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 83
 QY 61 ELVDCASQHGCHGDTTPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
 DB 84 ELVDCASQHGCHGDTTPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 143
 QY 121 PPANKIREALQTHSAIAVIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 180
 DB 144 PPANKIREALQTHSAIAVIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 203
 QY 181 QGVDDYWIVRNSWDTNWGDNGYGYFAANIDLMIMEEYPYVVIL 222
 DB 204 QGVDDYWIVRNSWDTNWGDNGYGYFAANIDLMIMEEYPYVVIL 245

RESULT 7
 AAR66545
 ID AAR66545 standard; protein; 245 AA.

XX AC AAR66545;
 XX DT 25-MAR-2003 (revised)
 XX DT 31-JUL-1995 (first entry)
 XX DE Der p I allergen.
 XX KW Der p I; allergen; antigen; immunological tolerance; peptide;
 XX KW cryptic epitope.
 XX OS Dermatophagoides pteronyssinus.
 XX FH WO9427634-A1.
 XX PN 08-DEC-1994.
 XX PD 01-JUN-1994; 94WO-AU000292.
 XX PF 02-JUN-1993; 93US-00072832.
 XX PR


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PA (CHIL-) INST CHILD HEALTH RES.
XX Thomas WR;
XX WPI; 1995-022467/03.
XX N-PSDB; AAQ79618.
XX Inducing immunological tolerance with cryptic peptide - esp from allergen
XX or auto:antigen, esp admin orally.
XX Disclosure; Page 22-23; 38pp; English.
XX Immunological tolerance to a protein antigen may be induced by admin. of
XX a compsn. contg. at least one cryptic peptide derived from that antigen.
XX Bio mice were immunised with various Der p I peptides and then response
XX to Der p I and the peptides was measured in the presence of spleen
XX adherent cells. Peptides contg. amino acids 120-143 and 144-169 of Der p
XX I were positive i.e., they contained cryptic epitopes. The cDNA fragment
XX encoding amino acids 131-187 of Der p I was cloned into pGEX and
XX expressed in bacteria as a fusion protein with glutathione-S-transferase.
XX Mice were given orally 3 mg of this protein on 3 consecutive days, then 7
XX days later immunised subcutaneously with native Der p I in complete
XX Freund's adjuvant. Seven days later lymph nodes, stimulated with protein
XX or synthetic peptides, were assayed for lymphokines (IL-2). Mice given
XX the cryptic epitope had a much weaker response than those treated only
XX with buffer. (Updated on 25-MAR-2003 to correct FN field.)
XX SQ Sequence 245 AA;

Query Match 100.0%; Score 1206; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. No. 3.le-127;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNACISNGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 60
Db 24 TNACISNGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 83
Qy 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNQAFGISNYCOIY 120
Db 84 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNQAFGISNYCOIY 143
Qy 121 PPNAKIREALAOHTSAIAVIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 180
Db 144 PPNAKIREALAOHTSAIAVIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 203
Qy 181 QGVDDYWIVRNSWDTNWGDNGYGYFAANIDLMIMEEYPPVVIL 222
Db 204 QGVDDYWIVRNSWDTNWGDNGYGYFAANIDLMIMEEYPPVVIL 245

RESULT 8
AAW71908
ID AAW71908 standard; protein; 245 AA.
XX
XX AAW71908;
XX
XX 27-AUG-2003 (revised)
XX 25-MAR-2003 (revised)
XX 16-DEC-1998 (first entry)
XX
XX Dermatophagoides Der p I.
XX
XX genus Dermatophagoides; major protein allergen; T cell epitope; Der p I;
XX Der p II; Der f I; Der f II; house dust mite allergy.
XX
XX Dermatophagoides.
XX
XX US5820862-A.
XX
XX 13-OCT-1998.
XX
XX 07-JUN-1995; 95US-00482142.
XX

PR 14-APR-1993; 93WO-US003471.
PR 14-APR-1994; 94US-00227772.
PR 19-MAY-1995; 95US-00445307.
XX
XX (IMMU-) IMMULOGIC PHARM CORP.
XX
XX Franzen HM, Kuo M, Evans S, Garman RD, Greenstein JL, Chen X;
XX Shaked Z, Rogers BL;
XX
XX WPI; 1998-567590/48.
XX N-PSDB; AAV61384.
XX
XX Dermatophagoides allergen peptides - useful for treating house dust mite
XX allergy.
XX Disclosure; Col 69-72; 155pp; English.
XX
XX The present invention describes peptides for treating sensitivity to
XX house dust mite allergens from the genus Dermatophagoides. Peptides
XX within the scope of the invention comprise at least one T cell epitope,
XX or preferably at least two T cell epitopes of a protein allergen selected
XX from the allergens Der p I, Der p II, Der f I, or Der f II. The invention
XX also describes modified peptides having similar or enhanced therapeutic
XX properties as the corresponding, naturally occurring allergen, but having
XX reduced side effects. The present sequence represents Der p I from the
XX present invention. (Updated on 25-MAR-2003 to correct PR field.) (Updated
XX on 27-AUG-2003 to correct OS field.)
XX SQ Sequence 245 AA;

Query Match 100.0%; Score 1206; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. No. 3.le-127;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNACISNGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 60
Db 24 TNACISNGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 83
Qy 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNQAFGISNYCOIY 120
Db 84 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNQAFGISNYCOIY 143
Qy 121 PPNAKIREALAOHTSAIAVIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 180
Db 144 PPNAKIREALAOHTSAIAVIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 203
Qy 181 QGVDDYWIVRNSWDTNWGDNGYGYFAANIDLMIMEEYPPVVIL 222
Db 204 QGVDDYWIVRNSWDTNWGDNGYGYFAANIDLMIMEEYPPVVIL 245

RESULT 9
AAW50356
ID AAW50356 standard; protein; 245 AA.
XX
XX AAW50356;
XX
XX 25-JAN-2000 (first entry)
XX
XX Dermatophagoides sp. allergen Der p I protein fragment.
XX
XX Allergen; house dust mite; detection; sensitivity; T cell epitope;
XX screening; allergic disorder; asthma; rhinitis; ectopic dermatitis;
XX Der p I.
XX
XX Dermatophagoides sp.
XX
XX US5968526-A.
XX
XX 19-OCT-1999.
XX
XX 07-JUN-1995; 95US-00478572.
XX

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PR 14-APR-1994; 94US-00227772.
 PR 12-APR-1995; 95WO-US004481.
 PR 19-MAY-1995; 95US-00445307.
 XX (IMMU-) IMMULOGIC PHARM CORP.
 PA Garman RD, Greenstein JL, Rogers BL, Franzen HM, Shaked Z;
 PI Chen X, Evans S, Kuo M;
 XX WPI; 1999-590385/50.
 DR N-PSDB; AA223906.
 XX Screening individuals for allergic reactions to T cell epitopes of major
 PT allergens from house dust mites.
 PT Disclosure; Col 73-74; 158pp; English.
 XX This invention describes a novel method (I) for detecting whether an
 CC individual is sensitive to Dermatophagoides (house dust mites). The
 CC method involves detecting sensitivity to house dust mites in patients,
 CC comprising combining a blood sample from the individual with 1 or more
 CC isolated T cell epitopes of the protein allergens I and II (DP I) and
 CC (DP II) from Dermatophagoides (house dust mites). 32 T cell epitopes
 CC with varying, defined amino acids sequences (given in the specification)
 CC may be used in (I). The sample and allergens are combined under
 CC conditions appropriate for the binding of blood components with the
 CC polypeptides. The extent of binding is then indicative of the sensitivity
 CC of the patient to house dust mites. (I) may be used to screen individuals
 CC for sensitivity to Dermatophagoides (house dust mites). The house dust
 CC mite is a major cause of a variety of allergic disorders such as asthma,
 CC rhinitis and eczematoid dermatitis. This sequence represents the house dust
 CC mite allergen Der p I
 XX Sequence 245 AA;
 SQ
 Query Match 100.0%; Score 1206; DB 2; Length 245;
 Best Local Similarity 100.0%; Pred. No. 3.1e-127;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
 DB 24 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 83
 QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAORFGISNYCQIY 120
 DB 84 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAORFGISNYCQIY 143
 QY 121 PPNAKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQDNGYQPNYHVNIVGYNSA 180
 DB 144 PPNAKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQDNGYQPNYHVNIVGYNSA 203
 QY 181 QGVYDIYVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 222
 DB 204 QGVYDIYVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 245
 RESULT 10
 AAU18959
 ID AAU18959 standard; protein; 245 AA.
 XX AAU18959;
 XX 04-DEC-2001 (first entry)
 XX House dust mite allergen Der p I.
 DE House dust mite; allergenic protein; Der p I; Der p II; Der f I;
 KW Der f II; antiallergenic; immunostimulant; house dust mite allergy;
 KW T-cell epitope.
 XX Dermatophagoides pteronyssinus.
 OS US6268491-B1.

XX 31-JUL-2001.
 PD 07-JUN-1995; 95US-00484296.
 XX 16-OCT-1991; 91US-00777859.
 PR 08-MAY-1992; 92US-00881396.
 PR 14-APR-1993; 93WO-US003471.
 PR 14-APR-1994; 94US-00227772.
 PR 19-MAY-1995; 95US-00445307.
 XX (IMMU-) IMMULOGIC PHARM CORP.
 PA Garman RD, Greenstein JL, Kuo M, Rogers BL, Franzen HM, Chen X;
 PI Evans S, Shaked Z;
 XX WPI; 2001-549074/61.
 DR N-PSDB; AA330721.
 XX Peptides comprising T cell groups of the major allergens from
 PT Dermatophagoides (house dust mites), useful for treating house dust mite
 PT allergy in humans, and for diagnosing sensitivity to house dust mite
 PT protein allergens.
 XX Example 1; Col 73; 158pp; English.
 XX The invention relates to an isolated peptide of the major protein
 CC allergens of the genus Dermatophagoides, which comprises at least one T
 CC cell group of a protein allergen from Der p (DP) I, DP II, Der f (DF) I
 CC or DF II. The isolated peptide comprises at least two regions, each
 CC region comprising at least one T cell group of a protein allergen of the
 CC genus Dermatophagoides. The regions are derived from the same or
 CC different protein allergens of the genus Dermatophagoides. The peptides
 CC are useful for treating house dust mite allergy in humans. The peptides
 CC are also useful for detecting or diagnosing sensitivity to house dust
 CC mite protein allergens. The present peptides have similar or enhanced
 CC therapeutic properties as the naturally-occurring allergen, but have
 CC reduced side effects, and increased solubility and stability. The present
 CC sequence represents an allergenic protein from Dermatophagoides from
 CC which the T-cell epitope containing peptides are derived
 XX Sequence 245 AA;
 SQ
 Query Match 100.0%; Score 1206; DB 4; Length 245;
 Best Local Similarity 100.0%; Pred. No. 3.1e-127;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
 DB 24 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 83
 QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAORFGISNYCQIY 120
 DB 84 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAORFGISNYCQIY 143
 QY 121 PPNAKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQDNGYQPNYHVNIVGYNSA 180
 DB 144 PPNAKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQDNGYQPNYHVNIVGYNSA 203
 QY 181 QGVYDIYVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 222
 DB 204 QGVYDIYVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 245
 RESULT 11
 ABG71812
 ID ABG71812 standard; protein; 245 AA.
 XX ABG71812;
 XX 10-JAN-2003 (first entry)
 XX European house dust mite Der p I protein.

XX Dermatophagoides farinae protein allergen; Der f I; Der f II; allergic;
 KW allergic response; mite allergen; house dust mite; T cell epitope;
 KW B cell epitope; anti-allergic; desensitisation therapy;
 KW modifies allergic response of house dust mite-sensitive individual;
 KW modify B-cell and/or T-cell response to Der f I and Der f II;
 KW European house dust mite; Der p I.
 XX Dermatophagoides pteronyssinus.
 XX US6423837-B1.
 XX 23-JUL-2002.
 XX 20-APR-1999; 99US-00295188.
 XX 13-FEB-1990; 90US-00458642.
 PR 11-SEP-1990; 90US-00580655.
 PR 16-AUG-1993; 93US-00107332.
 PR 29-DEC-1993; 93US-00175071.
 XX (IMMU-) IMMULOGIC PHARM CORP.
 XX Thomas WR, Chua K;
 XX WPI; 2002-672946/72.
 DR N-PSDB; ABS56342.
 XX Novel isolated DNA encoding peptide from Dermatophagoides farinae protein
 PT allergen, designated Der f I and Der f II, useful for treating and
 PT preventing allergic responses to mite allergens, by desensitization
 PT therapy.
 XX Disclosure; Fig 7; 22pp; English.
 XX The present invention relates to a new DNA encoding a peptide from
 CC Dermatophagoides farinae protein allergen, designated Der f I or Der f
 CC II, that comprises at least one epitope of the protein allergen. The
 CC invention is useful for producing a peptide from Der f I or Der f II
 CC protein allergen. The invention is also useful for diagnosing, treating,
 CC and preventing allergic responses to mite allergens, particularly, the
 CC mites D. farinae. The invention is also useful as a probe for identifying
 CC additional nucleotide sequences coding for mite allergens having amino
 CC acid sequences similar to Der f I or Der f II. The peptide is useful for
 CC detecting sensitivity in an individual to house dust mites and can be
 CC used to treat sensitivity (reduce sensitivity or desensitize) in an
 CC individual, to whom therapeutically effective quantities of D. farinae
 CC peptide is administered. The peptides when administered to sensitive
 CC individual modify the individual's allergic response to Der f I or Der f
 CC II. The peptides are also useful as purified allergens useful in the
 CC standardisation of allergen extracts or preparations which can be used as
 CC reagents for diagnosis and treatment of allergy to house dust mites. The
 CC epitopic peptides are useful as diagnostic reagents for determining
 CC reactivity to the mite species. The peptides are also useful for
 CC identifying or defining T cell epitopes and/or B cell epitopes which are
 CC of importance in allergic responses to D. farinae allergens and to
 CC elucidate the mediators or mechanisms of by which these reactions occur.
 CC The present amino acid sequence represents the European house dust mite
 CC Der p I protein as described in the invention
 XX
 SQ Sequence 245 AA;
 Query Match 100.0%; Score 1206; DB 5; Length 245;
 Best Local Similarity 100.0%; Pred. No. 3.1e-127;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNACSSINGNAPAEIDLQRMFTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQLDLAEQ 60
 DB 24 TNACSSINGNAPAEIDLQRMFTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQLDLAEQ 83
 QY 61 ELVDCAHQHCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
 DB 84 ELVDCAHQHCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 143

QY 121 PPANKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 180
 DB 144 PPANKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 203
 QY 181 QGVYVIVRNSWDTNWDNGCYGYFAANIDLMIMIEEYPYVUIL 222
 DB 204 QGVYVIVRNSWDTNWDNGCYGYFAANIDLMIMIEEYPYVUIL 245
 RESULT 12
 AAR49920
 ID AAR49920 standard; protein; 320 AA.
 XX AAR49920;
 AC
 XX 25-MAR-2003 (revised)
 DT 17-OCT-1994 (first entry)
 XX Protein allergen of Der pI.
 DE Der pI; House Dust Mite Allergen.
 XX Dermatophagoides pteronyssinus.
 OS
 FH Key Location/Qualifiers
 FT Protein 1..322
 FT /label= Der pI preproenzyme
 FT Cleavage-site 83..85
 FT /label= Cleavage site
 FT /note= "proenzyme remains"
 FT Cleavage-site 85..97
 FT /label= cleavage site
 FT /note= "cleavage between pro-Der pI and pre-Der pI "
 XX WO9405790-A1.
 PN 17-MAR-1994.
 PD 10-SEP-1993; 93WO-US008518.
 PF 10-SEP-1992; 92US-00945288.
 PR (IMMU-) IMMULOGIC PHARM CORP.
 XX Thomas WR, Chua K;
 XX WPI; 1994-101195/12.
 DR N-PSDB; AAQ58665.
 XX New protein allergens of house dust mite - used for diagnosing and
 XX treating sensitivity in an individual to house dust mite allergens.
 XX Example 1; Fig 21; 98pp; English.
 XX AAR49920 is a preproenzyme Der pI. The amino acid sequence preceding the
 CC mature protein sequence contains cleavage sites for the pre- and
 CC proenzyme forms, with residues 1-97 corresponding to a partial signal
 CC peptide sequence. The mature protein can be used to detect sensitivity in
 CC an individual to house dust mite and to reduce the sensitivity of the
 CC individual. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 320 AA;
 Query Match 100.0%; Score 1206; DB 2; Length 320;
 Best Local Similarity 100.0%; Pred. No. 4.6e-127;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNACSSINGNAPAEIDLQRMFTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQLDLAEQ 60
 DB 99 TNACSSINGNAPAEIDLQRMFTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQLDLAEQ 158
 QY 61 ELVDCAHQHCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120

Db 159 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 218
 QY 121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
 Db 219 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 278
 QY 181 QGVVDYWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVVIL 222
 Db 279 QGVVDYWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVVIL 320

RESULT 13
 AAU07748
 ID AAU07748 standard; protein; 222 AA.
 XX
 AC AAU07748;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DE House dust mite allergenic protein Der p I variant d.
 XX
 KW House dust mite; allergenic protein; Der p I; Der p II; Der f I;
 KW Der f II; antiallergenic; immunostimulant; house dust mite allergy;
 KW T-cell epitope; polymorphic variant.
 XX
 OS Dermatophagoides pteronyssinus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 136
 FT /note= "Wild-type Ser substituted by Thr"
 XX
 PN US6268491-B1.
 XX
 PD 31-JUL-2001.
 XX
 PF 07-JUN-1995; 95US-00484296.
 XX
 PR 16-OCT-1991; 91US-00777859.
 PR 08-MAY-1992; 92US-00881396.
 PR 14-APR-1993; 93WO-US0003471.
 PR 14-APR-1994; 94US-00227772.
 PR 19-MAY-1995; 95US-00445307.
 XX
 PA (IMMU-) IMMULOGIC PHARM CORP.
 XX
 PI Garman RD, Greenstein JL, Kuo M, Rogers BL, Franzen HM, Chen X;
 PI Evans S, Shaked Z;
 XX
 DR WPI; 2001-549074/61.
 XX
 PT Peptides comprising T cell groups of the major allergens from
 PT Dermatophagoides (house dust mites), useful for treating house dust mite
 PT allergy in humans, and for diagnosing sensitivity to house dust mite
 PT protein allergens.
 XX
 PS Disclosure; Fig 22; 158pp; English.
 XX
 CC The invention relates to an isolated peptide of the major protein
 CC allergens of the genus Dermatophagoides, which comprises at least one T
 CC cell group of a protein allergen from Der p (DP) I, DP II, Der f (DF) I
 CC or DF II. The isolated peptide comprises at least two regions, each
 CC region comprising at least one T cell group of a protein allergen of the
 CC genus Dermatophagoides. The regions are derived from the same or
 CC different protein allergens of the genus Dermatophagoides. The peptides
 CC are useful for treating house dust mite allergy in humans. The peptides
 CC are also useful for detecting or diagnosing sensitivity to house dust
 CC mite protein allergens. The present peptides have similar or enhanced
 CC therapeutic properties as the naturally-occurring allergen, but have
 CC reduced side effects, and increased solubility and stability. The present
 CC sequence represents an allergenic protein from Dermatophagoides from
 CC which the T-cell epitope containing peptides are derived, a polymorphic
 CC variant of Der p I. Note: The present sequence is not shown in the

CC specification but is derived from the Der p I sequence shown in figure 22
 XX
 SQ Sequence 222 AA;
 Query Match 99.8%; Score 1203; DB 4; Length 222;
 Best Local Similarity 99.5%; Pred. No. 5.8e-127;
 Matches 221; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNACSSINGNAPAEIDLRQMRVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
 Db 1 TNACSSINGNAPAEIDLRQMRVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
 QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
 Db 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
 QY 121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
 Db 121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
 QY 181 QGVVDYWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVVIL 222
 Db 181 QGVVDYWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVVIL 222

RESULT 14
 AAB98347
 ID AAB98347 standard; protein; 222 AA.
 XX
 AC AAB98347;
 XX
 DT 21-AUG-2001 (first entry)
 XX
 DE D. pteronyssinus Der p 1 protein SEQ ID NO:82.
 XX
 KW Mite group 1 protein; methyltrophic yeast; Escherichia coli; allergy;
 KW recombinant mite group 1 protein; allergic response; antiallergic;
 KW infectious disease; allergic disease.
 XX
 OS Dermatophagoides pteronyssinus.
 XX
 PN WO200129078-A2.
 XX
 PD 26-APR-2001.
 XX
 PF 12-OCT-2000; 2000WO-US028204.
 XX
 PR 15-OCT-1999; 99US-0159841P.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Best EA, McDermott MJ;
 XX
 DR WPI; 2001-308475/32.
 DR N-PSDB; AAH22385.
 XX
 PT Producing recombinant mite Group 1 protein for treating allergies.
 PT involves culturing a methyltrophic yeast microorganism or Escherichia
 PT coli transformed with nucleic acid molecule, and recovering the protein.
 XX
 PS Claim 12; Page 145; 154pp; English.
 XX
 CC The present invention describes a method for the production of a
 CC recombinant mite Group 1 protein (I). The method comprises culturing a
 CC methyltrophic yeast microorganism transformed with a nucleic acid
 CC molecule (II) encoding (I), and recovering (I), or culturing Escherichia
 CC coli transformed with (II) under conditions in which (I) forms an
 CC inclusion body in E. coli, isolating the inclusion body, and recovering
 CC (I). Also described is a method for detecting mite allergy in an animal
 CC comprising: (a) contacting (I) with a putative IgE-containing substance
 CC to form a complex between (I) and IgE, and (b) determining the presence of
 CC of IgE reactive with (I) by detecting the complex, where the presence of
 CC reactive IgE is indicative of mite allergy in the animal. (I) is useful

CC for detecting mite allergy in an animal, or in a composition to reduce
 CC allergic response to a mite Group 1 protein in a mite allergic animal.
 CC (I) is also useful in a composition for treating or preventing allergic,
 CC infectious or other diseases. AAH22326 to AAH22394 and AAB98326 to
 CC AAB98349 represent sequences used in the exemplification of the present
 CC invention
 XX Sequence 222 AA;
 SQ Sequence 222 AA;
 Query Match 99.5%; Score 1200; DB 4; Length 222;
 Best Local Similarity 99.5%; Pred. No. 1.3e-126;
 Matches 221; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNACSSINGNAPAEIDLRQMTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 60
 DB 1 TNACSSINGNAPAEIDLRQMTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 60
 QY 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 120
 DB 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 120
 QY 121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYNA 180
 DB 121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYNA 180
 QY 181 QGVDTYWIVRNSWDTNWGDNGYGYFAANIDLMIEEYPYVIL 222
 DB 181 QGVDTYWIVRNSWDTNWGDNGYGYFAANIDLMIEEYPYVIL 222
 RESULT 15
 AAB98346
 ID AAB98346 standard; protein; 302 AA.
 XX AAB98346;
 XX 21-AUG-2001 (first entry)
 XX D. pteronyssinus Der p 1 protein SEQ ID NO:77.
 XX Mite group 1 protein; methyltrophic yeast; Escherichia coli; allergy;
 KW recombinant mite group 1 protein; allergic response; antiallergic;
 KW infectious disease; allergic disease.
 XX Dermatophagoides pteronyssinus.
 XX WO200129078-A2.
 XX 26-APR-2001.
 XX 12-OCT-2000; 2000WO-US028204.
 XX 15-OCT-1999; 99US-0159841P.
 XX (HESK-) HESKA CORP.
 XX Best EA, McDermott MJ;
 XX WPI; 2001-308475/32.
 XX N-PSDB; AAH22381.
 XX Producing recombinant mite Group 1 protein for treating allergies,
 PT involves culturing a methyltrophic yeast microorganism or Escherichia
 PT coli transformed with nucleic acid molecule, and recovering the protein.
 XX Claim 12; Page 141-142; 154pp; English.
 XX The present invention describes a method for the production of a
 CC recombinant mite Group 1 protein (I). The method comprises culturing a
 CC methyltrophic yeast microorganism transformed with a nucleic acid
 CC molecule (II) encoding (I), and recovering (I), or culturing Escherichia
 CC coli transformed with (II) under conditions in which (I) forms an
 CC inclusion body in E. coli, isolating the inclusion body, and recovering

CC (I). Also described is a method for detecting mite allergy in an animal
 CC comprising: (a) contacting (I) with a putative IGE-containing substance
 CC to form a complex between (I) and IGE; and (b) determining the presence
 CC of IGE reactive with (I) by detecting the complex, where the presence of
 CC reactive IGE is indicative of mite allergy in the animal. (I) is useful
 CC for detecting mite allergy in an animal, or in a composition to reduce
 CC allergic response to a mite Group 1 protein in a mite allergic animal.
 CC (I) is also useful in a composition for treating or preventing allergic,
 CC infectious or other diseases. AAH22326 to AAH22394 and AAB98326 to
 CC AAB98349 represent sequences used in the exemplification of the present
 CC invention
 XX Sequence 302 AA;
 SQ Sequence 302 AA;
 Query Match 99.5%; Score 1200; DB 4; Length 302;
 Best Local Similarity 99.5%; Pred. No. 2e-126;
 Matches 221; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNACSSINGNAPAEIDLRQMTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 60
 DB 81 TNACSSINGNAPAEIDLRQMTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 140
 QY 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 120
 DB 141 ELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 200
 QY 121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYNA 180
 DB 201 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYNA 260
 QY 181 QGVDTYWIVRNSWDTNWGDNGYGYFAANIDLMIEEYPYVIL 222
 DB 261 QGVDTYWIVRNSWDTNWGDNGYGYFAANIDLMIEEYPYVIL 302

Search completed: May 19, 2005, 17:21:37
 Job time : 166 secs

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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:23:37 ; Search time 132 Seconds
(without alignments)

562.581 Million cell updates/sec

Title: US-09-867-159A-2

Perfect score: 1206

Sequence: 1 TNACSSINGNAPAEIDLQRM.....YFAANIDLMMEBYPYVIL 222

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1206	100.0	222	10	US-09-867-159A-2
2	1196	99.2	222	14	US-10-001-245-88
3	1196	99.2	320	9	US-09-877-160-2
4	1196	99.2	320	10	US-09-847-208-79
5	1196	99.2	320	14	US-10-001-245-179
6	1190	98.7	302	17	US-10-892-543-8
7	1186	98.3	303	17	US-10-892-543-32
8	1180	97.8	302	17	US-10-892-543-11
9	1176	97.5	303	17	US-10-892-543-20
10	1176	97.5	303	17	US-10-892-543-35
11	1176	97.5	303	17	US-10-892-543-38
12	1170	97.0	302	17	US-10-892-543-14
13	1166	96.7	303	17	US-10-892-543-41

14	1162	96.4	222	14	US-10-001-245-26	Sequence 26, Appl
15	1161	96.3	222	14	US-10-001-245-18	Sequence 18, Appl
16	1161	96.3	222	14	US-10-001-245-20	Sequence 20, Appl
17	1161	96.3	222	14	US-10-001-245-24	Sequence 24, Appl
18	1160	96.2	218	17	US-10-892-543-5	Sequence 5, Appl
19	1160	96.2	298	17	US-10-892-543-2	Sequence 2, Appl
20	1159	96.1	222	14	US-10-001-245-22	Sequence 22, Appl
21	1157	95.9	222	14	US-10-001-245-14	Sequence 14, Appl
22	1157	95.9	222	14	US-10-001-245-16	Sequence 16, Appl
23	1156	95.9	299	17	US-10-892-543-23	Sequence 23, Appl
24	1150	95.4	296	17	US-10-892-543-17	Sequence 17, Appl
25	1146	95.0	297	17	US-10-892-543-29	Sequence 29, Appl
26	1146	95.0	299	17	US-10-892-543-26	Sequence 26, Appl
27	1143	94.8	222	14	US-10-001-245-30	Sequence 30, Appl
28	1142	94.7	222	14	US-10-001-245-28	Sequence 28, Appl
29	1133	93.9	222	14	US-10-001-245-34	Sequence 34, Appl
30	1132	93.9	222	14	US-10-001-245-32	Sequence 32, Appl
31	1040.5	86.3	327	14	US-10-001-245-182	Sequence 182, App
32	1037.5	86.0	246	14	US-10-001-245-181	Sequence 181, App
33	1037.5	86.0	321	14	US-10-001-245-180	Sequence 180, App
34	997.5	82.7	321	10	US-09-847-208-73	Sequence 73, Appl
35	997.5	82.7	321	14	US-10-001-245-183	Sequence 183, App
36	982.5	81.5	211	10	US-09-847-208-95	Sequence 95, Appl
37	982.5	81.5	211	14	US-10-001-245-184	Sequence 184, App
38	944.5	78.3	210	14	US-10-001-245-185	Sequence 185, App
39	332.5	27.6	357	16	US-10-437-963-135411	Sequence 135411,
40	332.5	27.6	696	14	US-10-259-165-184	Sequence 184, App
41	331	27.4	363	15	US-10-425-114-48978	Sequence 48978, A
42	324.5	26.9	249	15	US-10-425-114-44401	Sequence 44401, A
43	324.5	26.9	381	15	US-10-425-114-43777	Sequence 43777, A
44	323.5	26.8	329	9	US-09-953-956-2	Sequence 2, Appl
45	323.5	26.8	329	13	US-10-114-464-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-867-159A-2
Sequence 2, Application US/09867159A

Publication No. US20030104013A1

GENERAL INFORMATION:

APPLICANT: ANTIALIS

TERRASSE, GASTAN

LORIA, EMILE

TREHIN, YVES

TITLE OF INVENTION: Anti-allergic pharmaceutical composition containing at least one

and at least one anti-histamine compound

FILE REFERENCE: B112812US-antialis

FILE REFERENCE: B112812US-antialis

CURRENT APPLICATION NUMBER: US/09/867,159A

PRIOR FILING DATE: 2001-05-29

PRIOR APPLICATION NUMBER: FR01/04370

PRIOR FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: FR01/05929

PRIOR FILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 222

TYPE: PRT

ORGANISM: Dermatophagoides pteronyssinus

FEATURE:

NAME/KEY: PEPTIDE

LOCATION: (1)..(222)

OTHER INFORMATION: Peptide sequence from cystine protease.

US-09-867-159A-2

Query Match 100.0%; Score 1206; DB 10; Length 222;

Best Local Similarity 100.0%; Pred. No. 1.3e-118; Indels 0; Gaps 0;

Matches 222; Conservative 0; Mismatches 0;

Qy 1 TNACSSINGNAPAEIDLQRMRTVTPIRMGGCGGSCWAFSGVAATESAYLAHNRQSLDLAEQ 60

Db 1 TNACSSINGNAPAEIDLQRMRTVTPIRMGGCGGSCWAFSGVAATESAYLAHNRQSLDLAEQ 60

Qy 61 ELVDCASQHGCHGTIPRGIEYIOHNGVVOESYTRYVAREQSCRPNARFGISNYCQIY 120

Db 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-877-160-2
Query Match 99.2%; Score 1196; DB 14; Length 222;
Best Local Similarity 99.1%; Pred. No. 1.4e-117;
Matches 220; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 121 PPNANKIREALAOQTHSAIAVIGIKDLDAFRHYDGRITIIORDNGYQPNYHAVNIVGYSNA 180
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-877-160-2
Db 121 PPNANKIREALAOQTHSAIAVIGIKDLDAFRHYDGRITIIORDNGYQPNYHAVNIVGYSNA 180
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-877-160-2
Qy 181 QGVDYWI VRNSWDTNWGDNGYGYFAANIDLMIMEEYPYVVIL 222
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-877-160-2
Db 181 QGVDYWI VRNSWDTNWGDNGYGYFAANIDLMIMEEYPYVVIL 222
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-877-160-2

RESULT 2

US-10-001-245-88
; Sequence 88, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; PRIOR FILING DATE: 2001-11-15
; PRIOR FILING DATE: 2001-06-14
; PRIOR FILING DATE: 2001-06-14
; PRIOR FILING DATE: 2001-06-14
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 88
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-88

Query Match 99.2%; Score 1196; DB 14; Length 222;
Best Local Similarity 99.1%; Pred. No. 1.4e-117;
Matches 220; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TNACSGINGNAPAEIDLRQMTVTPIRMQCGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Db 1 TNACSGINGNAPAEIDLRQMTVTPIRMQCGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Qy 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Db 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Qy 121 PPNANKIREALAOQTHSAIAVIGIKDLDAFRHYDGRITIIORDNGYQPNYHAVNIVGYSNA 180
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Db 121 PPNANKIREALAOQTHSAIAVIGIKDLDAFRHYDGRITIIORDNGYQPNYHAVNIVGYSNA 180
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Qy 181 QGVDYWI VRNSWDTNWGDNGYGYFAANIDLMIMEEYPYVVIL 222
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Db 181 QGVDYWI VRNSWDTNWGDNGYGYFAANIDLMIMEEYPYVVIL 222
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79

RESULT 3

US-09-877-160-2
; Sequence 2, Application US/09877160
; Publication No. US20020197268A1
; GENERAL INFORMATION:
; APPLICANT: Ching-Huang, Hsu
; APPLICANT: Cheng, Winston T. K.
; TITLE OF INVENTION: ALLERGEN-CONTAINING MILK FOR ALLERGY
; FILE REFERENCE: 12774-003001
; CURRENT APPLICATION NUMBER: US/09/877,160
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2

; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-877-160-2
Query Match 99.2%; Score 1196; DB 9; Length 320;
Best Local Similarity 99.1%; Pred. No. 2.3e-117;
Matches 220; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TNACSGINGNAPAEIDLRQMTVTPIRMQCGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-877-160-2
Db 99 TNACSGINGNAPAEIDLRQMTVTPIRMQCGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 158
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-877-160-2
Qy 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Db 159 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 218
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Qy 121 PPNANKIREALAOQTHSAIAVIGIKDLDAFRHYDGRITIIORDNGYQPNYHAVNIVGYSNA 180
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Db 219 PPNANKIREALAOQTHSAIAVIGIKDLDAFRHYDGRITIIORDNGYQPNYHAVNIVGYSNA 278
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Qy 181 QGVDYWI VRNSWDTNWGDNGYGYFAANIDLMIMEEYPYVVIL 222
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Db 279 QGVDYWI VRNSWDTNWGDNGYGYFAANIDLMIMEEYPYVVIL 320
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79

RESULT 4

US-09-847-208-79
; Sequence 79, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; FILE REFERENCE: 19E-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus (House-dust mite)
US-09-847-208-79

Query Match 99.2%; Score 1196; DB 10; Length 320;
Best Local Similarity 99.1%; Pred. No. 2.3e-117;
Matches 220; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TNACSGINGNAPAEIDLRQMTVTPIRMQCGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Db 99 TNACSGINGNAPAEIDLRQMTVTPIRMQCGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 158
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Qy 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Db 159 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 218
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Qy 121 PPNANKIREALAOQTHSAIAVIGIKDLDAFRHYDGRITIIORDNGYQPNYHAVNIVGYSNA 180
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Db 219 PPNANKIREALAOQTHSAIAVIGIKDLDAFRHYDGRITIIORDNGYQPNYHAVNIVGYSNA 278
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Qy 181 QGVDYWI VRNSWDTNWGDNGYGYFAANIDLMIMEEYPYVVIL 222
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79
Db 279 QGVDYWI VRNSWDTNWGDNGYGYFAANIDLMIMEEYPYVVIL 320
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-847-208-79

RESULT 5

US-10-001-245-179
; Sequence 179, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:

; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1el mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 179
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-179

Query Match 99.2%; Score 1196; DB 14; Length 320;
Best Local Similarity 99.1%; Pred. No. 2.3e-117;
Matches 220; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TNACSGNAPAEIDLQMTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
Db 99 TNACSGNAPAEIDLQMTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 158
Qy 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCOIY 120
Db 159 ELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCOIY 218
Qy 121 PPNANKIREALAQTHSAIAVIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 180
Db 219 PPNVKNIREALAQTHSAIAVIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 278
Qy 181 QGVYWIWRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 222
Db 279 QGVYWIWRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 320

RESULT 6
US-10-892-543-8
; Sequence 8, Application US/10892543
; Publication No. US20050053615A1
; GENERAL INFORMATION:
; APPLICANT: Best, Elaine A.
; APPLICANT: McDermott, Martin J.
; TITLE OF INVENTION: VARIANTS OF MITE GROUP 1 ALLERGENS FOR THE TREATMENT OF HOUSE
; FILE REFERENCE: AL-10
; CURRENT APPLICATION NUMBER: US/10/892,543
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: 60/487,812
; PRIOR FILING DATE: 2003-07-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-892-543-8

Query Match 98.7%; Score 1190; DB 17; Length 302;
Best Local Similarity 99.1%; Pred. No. 9.2e-117;
Matches 220; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TNACSGNAPAEIDLQMTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
Db 81 TNACSGNAPAEIDLQMTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 140
Qy 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCOIY 120

Db 141 ELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCOIY 200
Qy 121 PPNANKIREALAQTHSAIAVIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 180
Db 201 PPNANKIREALAQTHSAIAVIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 260
Qy 181 QGVYWIWRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 222
Db 261 QGVYWIWRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 302

RESULT 7
US-10-892-543-32
; Sequence 32, Application US/10892543
; Publication No. US20050053615A1
; GENERAL INFORMATION:
; APPLICANT: Best, Elaine A.
; APPLICANT: McDermott, Martin J.
; TITLE OF INVENTION: VARIANTS OF MITE GROUP 1 ALLERGENS FOR THE TREATMENT OF HOUSE
; FILE REFERENCE: AL-10
; CURRENT APPLICATION NUMBER: US/10/892,543
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: 60/487,812
; PRIOR FILING DATE: 2003-07-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-892-543-32

Query Match 98.3%; Score 1186; DB 17; Length 303;
Best Local Similarity 98.6%; Pred. No. 2.4e-116;
Matches 219; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TNACSGNAPAEIDLQMTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
Db 82 TNACSGNAPAEIDLQMTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 141
Qy 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCOIY 120
Db 142 ELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCOIY 201
Qy 121 PPNANKIREALAQTHSAIAVIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 180
Db 202 PPNANKIREALAQTHSAIAVIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 261
Qy 181 QGVYWIWRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 222
Db 262 QGVYWIWRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 303

RESULT 8
US-10-892-543-11
; Sequence 11, Application US/10892543
; Publication No. US20050053615A1
; GENERAL INFORMATION:
; APPLICANT: Best, Elaine A.
; APPLICANT: McDermott, Martin J.
; TITLE OF INVENTION: VARIANTS OF MITE GROUP 1 ALLERGENS FOR THE TREATMENT OF HOUSE
; FILE REFERENCE: AL-10
; CURRENT APPLICATION NUMBER: US/10/892,543
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: 60/487,812
; PRIOR FILING DATE: 2003-07-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 302
; TYPE: PRT

```
; ORGANISM: Dermatophagoides pteronyssinus
US-10-892-543-11

Query Match
Best Local Similarity 97.8%; Score 1180; DB 17; Length 302;
Matches 219; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TNACSTNGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAAATESAYLAHRNOSLDLAEQ 60
Db 81 TNASSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAAATESAYLAHRNOSLDLAEQ 140

QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 120
Db 141 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 200

QY 121 PPNANKIREALAOQTHSAIAVIGIKOLDAPRHYDGRITIIQORDNGYQPNYHAVNIVGYSNA 180
Db 201 PPNANKIREALAOQTHSAIAVIGIKOLDAPRHYDGRITIIQORDNGYQPNYHAVNIVGYSNA 260

QY 181 QGVDDYWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVVIL 222
Db 261 QGVDDYWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVVIL 302

RESULT 9
US-10-892-543-20
; Sequence 20, Application US/10892543
; Publication No. US20050053615A1
; GENERAL INFORMATION:
; APPLICANT: Best, Elaine A.
; TITLE OF INVENTION: VARIANTS OF MITE GROUP 1 ALLERGENS FOR THE TREATMENT OF HOUSE
; TITLE OF INVENTION: DUST MITE ALLERGY
; FILE REFERENCE: AL-10
; CURRENT APPLICATION NUMBER: US/10/892,543
; CURRENT FILING DATE: 2004-07-15
; PRIOR FILING DATE: 2003-07-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-892-543-20

Query Match
Best Local Similarity 97.5%; Score 1176; DB 17; Length 303;
Matches 218; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TNACSTNGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAAATESAYLAHRNOSLDLAEQ 60
Db 82 TNASSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAAATESAYLAHRNOSLDLAEQ 141

QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 120
Db 142 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 201

QY 121 PPNANKIREALAOQTHSAIAVIGIKOLDAPRHYDGRITIIQORDNGYQPNYHAVNIVGYSNA 180
Db 202 PPNANKIREALAOQTHSAIAVIGIKOLDAPRHYDGRITIIQORDNGYQPNYHAVNIVGYSNA 261

QY 181 QGVDDYWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVVIL 222
Db 262 QGVDDYWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVVIL 303

RESULT 10
US-10-892-543-35
; Sequence 35, Application US/10892543
; Publication No. US20050053615A1
; GENERAL INFORMATION:
; APPLICANT: Best, Elaine A.
; TITLE OF INVENTION: VARIANTS OF MITE GROUP 1 ALLERGENS FOR THE TREATMENT OF HOUSE
; TITLE OF INVENTION: DUST MITE ALLERGY
; FILE REFERENCE: AL-10
; CURRENT APPLICATION NUMBER: US/10/892,543
; CURRENT FILING DATE: 2004-07-15
; PRIOR FILING DATE: 2003-07-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-892-543-35

Query Match
Best Local Similarity 97.5%; Score 1176; DB 17; Length 303;
Matches 218; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TNACSTNGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAAATESAYLAHRNOSLDLAEQ 60
Db 82 TNASSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAAATESAYLAHRNOSLDLAEQ 141

QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 120
Db 142 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 201

QY 121 PPNANKIREALAOQTHSAIAVIGIKOLDAPRHYDGRITIIQORDNGYQPNYHAVNIVGYSNA 180
Db 202 PPNANKIREALAOQTHSAIAVIGIKOLDAPRHYDGRITIIQORDNGYQPNYHAVNIVGYSNA 261

QY 181 QGVDDYWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVVIL 222
Db 262 QGVDDYWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVVIL 303

RESULT 11
US-10-892-543-38
; Sequence 38, Application US/10892543
; Publication No. US20050053615A1
; GENERAL INFORMATION:
; APPLICANT: Best, Elaine A.
; TITLE OF INVENTION: VARIANTS OF MITE GROUP 1 ALLERGENS FOR THE TREATMENT OF HOUSE
; TITLE OF INVENTION: DUST MITE ALLERGY
; FILE REFERENCE: AL-10
; CURRENT APPLICATION NUMBER: US/10/892,543
; CURRENT FILING DATE: 2004-07-15
; PRIOR FILING DATE: 2003-07-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-892-543-38

Query Match
Best Local Similarity 97.5%; Score 1176; DB 17; Length 303;
Matches 218; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TNACSTNGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAAATESAYLAHRNOSLDLAEQ 60
Db 82 TNASSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAAATESAYLAHRNOSLDLAEQ 141

QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 120
Db 142 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 201

QY 121 PPNANKIREALAOQTHSAIAVIGIKOLDAPRHYDGRITIIQORDNGYQPNYHAVNIVGYSNA 180
Db 202 PPNANKIREALAOQTHSAIAVIGIKOLDAPRHYDGRITIIQORDNGYQPNYHAVNIVGYSNA 261

QY 181 QGVDDYWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVVIL 222
Db 262 QGVDDYWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVVIL 303
```

Best Local Similarity 97.7%; Pred. No. 3.1e-114;
Matches 217; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TNACSGNAPAEIDLQRMTVTPIRMQCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
Db 82 TNASSINGNAPAEIDLQRMTVTPIRMQCGSCWAFSGVAATESAYLAHRNQSLLAEQ 141
Qy 61 ELVDCASQHGCHGDTTPRGIEYIQHNGVVQESYRYVAREQSCRRPNARFGISNYCQIY 120
Db 142 ELVDCASQHGCHGDTTPRGIEYIQHNGVVQESYRYVAREQSCRRPNARFGISNYCQIY 201
Qy 121 PPANKIRALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGSNA 180
Db 202 PPNVNKIRALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGSNA 261
Qy 181 QGVYDWIVNSWDTNMGDNGYGYFAANIDLMIMEEYPPVVIL 222
Db 262 QGVYDWIVNSWDTNMGDNGYGYFAANIDLMIMEEYPPVVIL 303

RESULT 14
US-10-001-245-26
; Sequence 26, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens
; FILE REFERENCE: 4305/IH942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-26

Query Match 96.4%; Score 1162; DB 14; Length 222;
Best Local Similarity 96.4%; Pred. No. 5.5e-114;
Matches 214; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TNACSGNAPAEIDLQRMTVTPIRMQCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
Db 1 TNACSGNAPAEIDLQRMTVTPIRMQCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
Qy 61 ELVDCASQHGCHGDTTPRGIEYIQHNGVVQESYRYVAREQSCRRPNARFGISNYCQIY 120
Db 61 ELVDCANQHGCHGDTTPRGIEYIQHNGVVQESYRYVAREQSCRRPNARFGISNYCQIY 120
Qy 121 PPANKIRALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGSNA 180
Db 121 PPNVNKIRALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGSNA 180
Qy 181 QGVYDWIVNSWDTNMGDNGYGYFAANIDLMIMEEYPPVVIL 222
Db 181 QGVYDWIVNSWDTNMGDNGYGYFAANIDLMIMEEYPPVVIL 222

RESULT 15
US-10-001-245-18
; Sequence 18, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik

; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1el mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-18

Query Match 96.3%; Score 1161; DB 14; Length 222;
Best Local Similarity 96.4%; Pred. No. 7e-114;
Matches 214; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
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Db |||||
Qy 1 TNACSSINGNAPAEIDLROMETVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
Db |||||
Qy 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREOSCCRPNRQFISNYCQIY 120
Db |||||
Qy 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREOSCCRPNRQFISNYCQIY 120
Db |||||
Qy 121 PPNANKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
Db |||||
Qy 121 PPNANKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
Db |||||
Qy 181 QGVDTYIVRNSWDTNMGDNGYGYFAANIDLMMIEEYPYVIVL 222
Db |||||
Qy 181 QGVDTYIVRNSWDTNMGDNGYGYFAANIDLMMIEEYPYVIVL 222
Db |||||

Search completed: May 19, 2005, 17:35:46
Job time : 133 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:21:46 ; Search time 43 Seconds
(without alignments)
385.397 Million cell updates/sec

Title: US-09-867-159a-2

Perfect score: 1206

Sequence: 1 TNACSLNGNAPABIDLRQMR.....YFAANIDLMMEIYPYVWIL 222

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1206	100.0	245	1	US-07-945-288-2
2	1206	100.0	245	1	US-08-482-831-2
3	1206	100.0	245	1	US-08-461-809-2
4	1206	100.0	245	1	US-08-461-441-2
5	1206	100.0	245	2	US-08-482-142-2
6	1206	100.0	245	2	US-08-478-572-2
7	1206	100.0	245	3	US-08-484-296-2
8	1206	100.0	245	5	PCT-US93-08518-2
9	1206	100.0	320	1	US-07-945-288-10
10	1206	100.0	320	1	US-08-462-831-10
11	1206	100.0	320	1	US-08-461-809-10
12	1206	100.0	320	1	US-08-461-441-10
13	1206	100.0	320	5	PCT-US93-08518-10
14	1177	97.6	222	1	US-07-945-288-11
15	1177	97.6	222	1	US-08-462-831-11
16	1177	97.6	222	1	US-08-461-809-11
17	1177	97.6	222	1	US-08-461-441-11
18	1177	97.6	222	5	PCT-US93-08518-11
19	1144	94.9	245	3	US-08-460-040-2
20	997.5	82.7	321	1	US-07-945-288-6
21	997.5	82.7	321	1	US-08-462-831-6
22	997.5	82.7	321	1	US-08-461-809-6
23	997.5	82.7	321	2	US-08-461-441-6
24	997.5	82.7	321	2	US-08-482-142-6
25	997.5	82.7	321	2	US-08-478-572-6
26	997.5	82.7	321	3	US-08-484-296-6
27	997.5	82.7	321	5	PCT-US93-08518-6

Sequence 195, App
Sequence 195, App
Sequence 195, App
Sequence 197, App
Sequence 197, App
Sequence 197, App
Sequence 197, App
Sequence 2, Appli
Sequence 2, Appli
Sequence 20, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 36, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-07-945-288-2
; Sequence 2, Application US/07945288
; Patent No. 5433948
; GENERAL INFORMATION:
; APPLICANT: Thomas, Wayne R.
; APPLICANT: Chua, Kaw-Yan
; TITLE OF INVENTION: CLONING AND SEQUENCING OF ALLERGENS FROM
; TITLE OF INVENTION: DERMATOPHAGOIDES (HOUSE DUST MITES)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/945,288
; FILING DATE: 19920910
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 580,655
; FILING DATE: 11 SEPTEMBER 1990
; APPLICATION NUMBER: 458,642
; FILING DATE: 13 FEBRUARY 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDRAGOURAS, AMY E.
; REGISTRATION NUMBER: P36,207
; REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-945-288-2

Query Match 100.0%; Score 1206; DB 1; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.4e-129;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNACSNAGAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
Db 24 TNACSNAGAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 83
QY 61 ELVDCASQHGCHGDTTPRGIEYIQHNGVVOESYRYRVAREQSCRRPNAQRFGISNYCQIY 120
Db 84 ELVDCASQHGCHGDTTPRGIEYIQHNGVVOESYRYRVAREQSCRRPNAQRFGISNYCQIY 143
QY 121 PPANKIREALAOHTSAIAVIIGIKDLDAFRHYDGRITIIORDNGYQPNYHAVNIVGYSNA 180
Db 144 PPANKIREALAOHTSAIAVIIGIKDLDAFRHYDGRITIIORDNGYQPNYHAVNIVGYSNA 203
QY 181 QGVYWIVRNSWDTNWDNGYGYFAANIDLMIMIEEYPYVVIL 222
Db 204 QGVYWIVRNSWDTNWDNGYGYFAANIDLMIMIEEYPYVVIL 245

RESULT 2

US-08-462-831-2
; Sequence 2, Application US/08462831
; Patent No. 5552142
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
; TITLE OF INVENTION: DERMATOPHAGOIDES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,831
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/945,288
; FILING DATE: 10 SEPTEMBER 1992
; APPLICATION NUMBER: US 580,655
; FILING DATE: 11 SEPTEMBER 1990
; APPLICATION NUMBER: US 458,642
; FILING DATE: 13 FEBRUARY 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDRAGOURAS, AMY E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-462-831-2

Query Match 100.0%; Score 1206; DB 1; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.4e-129;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNACSNAGAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
Db 24 TNACSNAGAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 83
QY 61 ELVDCASQHGCHGDTTPRGIEYIQHNGVVOESYRYRVAREQSCRRPNAQRFGISNYCQIY 120

Db 84 ELVDCASQHGCHGDTTPRGIEYIQHNGVVOESYRYRVAREQSCRRPNAQRFGISNYCQIY 143
QY 121 PPANKIREALAOHTSAIAVIIGIKDLDAFRHYDGRITIIORDNGYQPNYHAVNIVGYSNA 180
Db 144 PPANKIREALAOHTSAIAVIIGIKDLDAFRHYDGRITIIORDNGYQPNYHAVNIVGYSNA 203
QY 181 QGVYWIVRNSWDTNWDNGYGYFAANIDLMIMIEEYPYVVIL 222
Db 204 QGVYWIVRNSWDTNWDNGYGYFAANIDLMIMIEEYPYVVIL 245

RESULT 3

US-08-461-809-2
; Sequence 2, Application US/08461809
; Patent No. 5770202
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
; TITLE OF INVENTION: DERMATOPHAGOIDES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,809
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/945,288
; FILING DATE: 10 SEPTEMBER 1992
; APPLICATION NUMBER: US 580,655
; FILING DATE: 11 SEPTEMBER 1990
; APPLICATION NUMBER: US 458,642
; FILING DATE: 13 FEBRUARY 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDRAGOURAS, AMY E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Query Match 100.0%; Score 1206; DB 1; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.4e-129;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNACSNAGAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
Db 24 TNACSNAGAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 83
QY 61 ELVDCASQHGCHGDTTPRGIEYIQHNGVVOESYRYRVAREQSCRRPNAQRFGISNYCQIY 120
Db 84 ELVDCASQHGCHGDTTPRGIEYIQHNGVVOESYRYRVAREQSCRRPNAQRFGISNYCQIY 143
QY 121 PPANKIREALAOHTSAIAVIIGIKDLDAFRHYDGRITIIORDNGYQPNYHAVNIVGYSNA 180


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RESULT 5
US-08-482-142-2
; Sequence 2, Application US/08482142
; Patent No. 5820862
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,142
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,307
; FILING DATE: 07 June 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.6US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-142-2

Query Match 100.0%; Score 1206; DB 2; Length 245
Best Local Similarity 100.0%; Pred. No. 1.4e-129;
Matches 222; Conservative 0; Mismatches 0; Indels

Qy 1 TNACSSINGNAPAEIDLQRMTVTPIRMQGCSCWAFSGVAAATESAYLAHRH
Db 24 TNACSSINGNAPAEIDLQRMTVTPIRMQGCSCWAFSGVAAATESAYLAHRH
Qy 61 ELVDCASQHCCHGDTTPRGLEYI OHNGVVQESYRVRVAREQSCRRRPNQARF
Db 84 ELVDCASQHCCHGDTTPRGLEYI OHNGVVQESYRVRVAREQSCRRRPNQARF
Qy 121 PPNANKIREALAOATHSAIAVIIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHA
Db 144 PPNANKIREALAOATHSAIAVIIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHA
Qy 181 QGVYDWI VRNSWDTNMGDNGYGYFAANIDLMITEEYPYVIL 222
Db 204 QGVYDWI VRNSWDTNMGDNGYGYFAANIDLMITEEYPYVIL 245

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RESULT 6
US-08-478-572-2
; Sequence 2, Application US/08478572
; Patent No. 5988526
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,572
; FILING DATE: 07-June-1995
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/445,307
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.605
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-478-572-2

Query Match 100.0%; Score 1206; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.4e-129;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNACSGNAPAEIDLQRMRTVTPIRMQCGSCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
DB 24 TNACSGNAPAEIDLQRMRTVTPIRMQCGSCGSCWAFSGVAATESAYLAHRNQSLLAEQ 83
QY 61 ELVDCASQHGCHGDTTPRGIEYIQHNGVVOESYRYVAREQSCRRPNAORFGISNYCOIY 120
DB 84 ELVDCASQHGCHGDTTPRGIEYIQHNGVVOESYRYVAREQSCRRPNAORFGISNYCOIY 143
QY 121 PPANKIREALAQTHSAIAVIIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYSNA 180
DB 144 PPANKIREALAQTHSAIAVIIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYSNA 203
QY 181 QGVYDWIVRNSWDTNWGDNGYGYFAANIDLMIMEEYPYVVIL 222
DB 204 QGVYDWIVRNSWDTNWGDNGYGYFAANIDLMIMEEYPYVVIL 245

RESULT 7
US-08-484-296-2

; Sequence 2, Application US/08484296
; Patent No. 6268491
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,296
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/445,307
; FILING DATE: 07 June 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.605
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-296-2

Query Match 100.0%; Score 1206; DB 3; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.4e-129;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNACSGNAPAEIDLQRMRTVTPIRMQCGSCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
DB 24 TNACSGNAPAEIDLQRMRTVTPIRMQCGSCGSCWAFSGVAATESAYLAHRNQSLLAEQ 83
QY 61 ELVDCASQHGCHGDTTPRGIEYIQHNGVVOESYRYVAREQSCRRPNAORFGISNYCOIY 120
DB 84 ELVDCASQHGCHGDTTPRGIEYIQHNGVVOESYRYVAREQSCRRPNAORFGISNYCOIY 143
QY 121 PPANKIREALAQTHSAIAVIIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYSNA 180
DB 144 PPANKIREALAQTHSAIAVIIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYSNA 203
QY 181 QGVYDWIVRNSWDTNWGDNGYGYFAANIDLMIMEEYPYVVIL 222
DB 204 QGVYDWIVRNSWDTNWGDNGYGYFAANIDLMIMEEYPYVVIL 245

RESULT 8
PCT-US93-08518-2
; Sequence 2, Application PC/TUS9308518
; GENERAL INFORMATION:

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;
; APPLICANT:
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
; TITLE OF INVENTION: DERMATOPHAGOIDES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08518
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/945,288
; FILING DATE: 10 SEPTEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDRAGOURAS, AMY E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-08518-2

Query Match 100.0%; Score 1206; DB 5; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.4e-129;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNACSSINGNAPAEIDLQMRITVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLLDAEQ 60
Db 24 TNACSSINGNAPAEIDLQMRITVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLLDAEQ 83
Qy 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCOIY 120
Db 84 ELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCOIY 143
Qy 121 PPNAKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYNSA 180
Db 144 PPNAKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYNSA 203
Qy 181 QGVDTYIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 222
Db 204 QGVDTYIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 245

RESULT 9
US-07-945-288-10
; Sequence 10, Application US/07945288
; Patent No. 5433948
; GENERAL INFORMATION:
; APPLICANT: Thomas, Wayne R.
; APPLICANT: Chua, Kaw-Yan
; TITLE OF INVENTION: CLONING AND SEQUENCING OF ALLERGENS FROM
; TITLE OF INVENTION: DERMATOPHAGOIDES (HOUSE DUST MITES)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
```

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;
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/945,288
; FILING DATE: 19920910
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 580,655
; FILING DATE: 11 SEPTEMBER 1990
; APPLICATION NUMBER: 458,642
; FILING DATE: 13 FEBRUARY 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDRAGOURAS, AMY E.
; REGISTRATION NUMBER: F36,207
; REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-945-288-10

Query Match 100.0%; Score 1206; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 2.1e-129;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNACSSINGNAPAEIDLQMRITVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLLDAEQ 60
Db 99 TNACSSINGNAPAEIDLQMRITVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLLDAEQ 158
Qy 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCOIY 120
Db 159 ELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCOIY 218
Qy 121 PPNAKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYNSA 180
Db 219 PPNAKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYNSA 278
Qy 181 QGVDTYIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 222
Db 279 QGVDTYIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVIL 320

RESULT 10
US-08-462-831-10
; Sequence 10, Application US/08462831
; Patent No. 5552142
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
; TITLE OF INVENTION: DERMATOPHAGOIDES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```



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; APPLICATION NUMBER: US 458,642
; FILING DATE: 13 FEBRUARY 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDRAGOURAS, AMY E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-08518-10
;
Query Match 100.0%; Score 1206; DB:1; Length 320;
Best Local Similarity 100.0%; Pred. No. 2.1e-129;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNACSSINGNAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNQSLLDLAEQ 60
Db 99 TNACSSINGNAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNQSLLDLAEQ 158
Qy 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNQAQRFGISNYCQIY 120
Db 159 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNQAQRFGISNYCQIY 218
Qy 121 PPNAKIREALAOQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYNSA 180
Db 219 PPNAKIREALAOQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYNSA 278
Qy 181 QGVDTWIVRNSWDTNWGDNGYGYFAANIDLMIMIEEYPVWVIL 222
Db 279 QGVDTWIVRNSWDTNWGDNGYGYFAANIDLMIMIEEYPVWVIL 320

RESULT 13
PCT-US93-08518-10
; Sequence 10, Application PC/TUS9308518
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
; TITLE OF INVENTION: DERMATOPHAGOIDES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08518
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/945,288
; FILING DATE: 10 SEPTEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDRAGOURAS, AMY E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-08518-10
;
Query Match 100.0%; Score 1206; DB:5; Length 320;
Best Local Similarity 100.0%; Pred. No. 2.1e-129;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNACSSINGNAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNQSLLDLAEQ 60
Db 99 TNACSSINGNAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNQSLLDLAEQ 158
Qy 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNQAQRFGISNYCQIY 120
Db 159 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNQAQRFGISNYCQIY 218
Qy 121 PPNAKIREALAOQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYNSA 180
Db 219 PPNAKIREALAOQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYNSA 278
Qy 181 QGVDTWIVRNSWDTNWGDNGYGYFAANIDLMIMIEEYPVWVIL 222
Db 279 QGVDTWIVRNSWDTNWGDNGYGYFAANIDLMIMIEEYPVWVIL 320

RESULT 14
US-07-945-288-11
; Sequence 11, Application US/07945288
; Patent No. 5433948
; GENERAL INFORMATION:
; APPLICANT: Thomas, Wayne R.
; APPLICANT: Chua, Kaw-Yan
; TITLE OF INVENTION: CLONING AND SEQUENCING OF ALLERGENS FROM
; TITLE OF INVENTION: DERMATOPHAGOIDES (HOUSE DUST MITES)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/945,288
; FILING DATE: 19920910
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 580,655
; FILING DATE: 11 SEPTEMBER 1990
; APPLICATION NUMBER: 458,642
; FILING DATE: 13 FEBRUARY 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDRAGOURAS, AMY E.
; REGISTRATION NUMBER: P36,207
; REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
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/ NAME/KEY: misc feature
/ LOCATION: 50
/ OTHER INFORMATION: /label=Xaa is His or Tyr
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/ NAME/KEY: misc feature
/ LOCATION: 81
/ OTHER INFORMATION: /label=Xaa is Glu or Lys
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 124
/ OTHER INFORMATION: /label=Xaa is Ala or Val
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 136
/ OTHER INFORMATION: /label=Xaa is Ser or Thr
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 215
/ OTHER INFORMATION: /label=Xaa is Glu or Gln
US-07-945-288-11

Query Match          97.6%; Score 1177; DB 1; Length 222;
Best Local Similarity 97.7%; Pred. No. 2.5e-126;
Matches 217; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 1 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAAATESAYLAHRNOSLDLAEQ 60

Qy 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 120
Db 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 120

Qy 121 PPNANKIREALAOETHSAIAVIIIGIKDLDAFRHYDGRITIIQDNGYQPNYHVNIVGYSNA 180
Db 121 PPNANKIREALAOETHSAIAVIIIGIKDLDAFRHYDGRITIIQDNGYQPNYHVNIVGYSNA 180

Qy 181 QGVDDYWIVRNSWDTNMGDNGYGFPAANIDLMMEIEEYPYVVIL 222
Db 181 QGVDDYWIVRNSWDTNMGDNGYGFPAANIDLMMEIEEYPYVVIL 222
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RESULT 15
US-08-462-831-11
; Sequence 11, Application US/08462831
; Patent No. 5552142
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
; TITLE OF INVENTION: DERMATOPHAGOIDES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,831
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/945,288
; FILING DATE: 10 SEPTEMBER 1992
; APPLICATION NUMBER: US 580,655
; FILING DATE: 11 SEPTEMBER 1990
; APPLICATION NUMBER: US 458,642
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/ FILING DATE: 13 FEBRUARY 1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MANDRAGOURAS, AMY E.
/ REGISTRATION NUMBER: 36,207
/ REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 227-7400
/ TELEFAX: (617) 227-5941
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 222 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 50
/ OTHER INFORMATION: /label=Xaa is His or Tyr
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 81
/ OTHER INFORMATION: /label=Xaa is Glu or Lys
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 124
/ OTHER INFORMATION: /label=Xaa is Ala or Val
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 136
/ OTHER INFORMATION: /label=Xaa is Ser or Thr
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 215
/ OTHER INFORMATION: /label=Xaa is Glu or Gln
US-08-462-831-11
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Query Match          97.6%; Score 1177; DB 1; Length 222;
Best Local Similarity 97.7%; Pred. No. 2.5e-126;
Matches 217; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAAATESAYLAHRNOSLDLAEQ 60
Db 1 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAAATESAYLAHRNOSLDLAEQ 60

Qy 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 120
Db 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 120

Qy 121 PPNANKIREALAOETHSAIAVIIIGIKDLDAFRHYDGRITIIQDNGYQPNYHVNIVGYSNA 180
Db 121 PPNANKIREALAOETHSAIAVIIIGIKDLDAFRHYDGRITIIQDNGYQPNYHVNIVGYSNA 180

Qy 181 QGVDDYWIVRNSWDTNMGDNGYGFPAANIDLMMEIEEYPYVVIL 222
Db 181 QGVDDYWIVRNSWDTNMGDNGYGFPAANIDLMMEIEEYPYVVIL 222
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Search completed: May 19, 2005, 17:32:32
Job time : 45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2005, 17:39:08 ; Search time 39 Seconds
(without alignments)
547.695 Million cell updates/sec

Title: US-09-867-159A-2
Perfect score: 1206
Sequence: 1 TNACSSINGNAPAEIDLQRMR.....YFAANIDLMWIEYPYVIL 222
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 114359

Minimum DB seq length: 0
Maximum DB seq length: 222

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	982.5	81.5	211	2 S21864	probable cysteine
2	389.5	32.3	94	2 S03380	major fecal allerg
3	315	26.1	215	2 A59428	ervatamin B (EC 3.
4	311	25.8	221	2 A59041	cysteine proteinas
5	301	25.0	216	2 S06837	glycyl endopeptida
6	298	24.7	218	1 KHCHL	cathepsin L (EC 3.
7	295	24.5	221	2 A59040	cysteine proteinas
8	284.5	23.6	217	2 S15844	cathepsin S (EC 3.
9	274	22.7	214	2 S46476	cysteine proteinas
10	273	22.6	218	2 S67481	cathepsin L-like c
11	240	19.9	212	2 S03964	stem bromelain (EC
12	209	17.3	183	2 A4938	cysteine proteinas
13	207	17.2	184	2 S02729	actinidain (EC 3.4
14	185.5	15.4	166	2 B4938	cysteine proteinas
15	179	14.8	95	2 PQ0650	senescence-associat
16	171	14.2	165	2 C44938	cysteine proteinas
17	156.5	13.0	139	2 A41404	cathepsin L (EC 3.
18	145	12.0	174	2 B48454	cathepsin B-like c
19	139	11.5	155	2 S57426	cysteine proteinas
20	129.5	10.7	110	2 A61061	actinidain (EC 3.4
21	129.5	10.7	157	2 S57451	cysteine proteinas
22	125.5	10.4	136	2 S57624	cysteine proteinas
23	123.5	10.2	152	2 S57425	cysteine proteinas
24	121	10.0	150	2 T25581	hypothetical prote
25	120.5	10.0	152	2 S57423	cysteine proteinas
26	116.5	9.7	152	2 S57421	cysteine proteinas
27	115	9.5	145	2 S60456	cysteine proteinas
28	111.5	9.2	30	2 B27634	major fecal allerg
29	111	9.2	152	2 S57422	cysteine proteinas

RESULT 1

S21864
Probable cysteine proteinase (EC 3.4.22.-) - Euroglyphus maynei
N;Alternate names: allergen Eur m 1
C;Species: Euroglyphus maynei
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S21864
R;Kent, N.A.; Hill, M.; Keen, J.N.; Holland, P.W.H.; Hart, B.
submitted to the EMBL Data Library, June 1991
A;Reference number: S21864
A;Accession: S21864
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-211 <KEN>
A;Cross-references: UNIPROT:P25780; EMBL:X60073
C;Genetics:
A;Introns: 100/3; 155/2
C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase

ALIGNMENTS

Query Match	81.5%;	Score 982.5;	DB 2;	Length 211;
Best Local Similarity	83.9%;	Pred. No. 4.3e-81;		
Matches	177;	Conservative	17;	Mismatches 16; Indels 1; Gaps 1;
Qy	1	TNACSSING-NAPAEIDLQRMTVTPIRMQCGSCWAFSGVAATESAYLAHRNQSLLAE	59	
Db	1	TYACSSINSVSLPSELDLRLTPTPIRMQCGSCWAFSGVASTESAYLAYRNMSLLAE	60	
Qy	60	QELVDCASQHGCHGDTIPRGIEYIQHNVVQESYYRYTVAREQSCRRPNAORFGISNYCQI	119	
Db	61	QELVDCASQHGCHGDTIPRGIEYIQQGVVQEHYYPYVAREQSCRRPNAORGYLKNYCQI	120	
Qy	120	YPNANKIREALAQTHSAIAVIIGIKDLDAFRHVDGRTTIQRDNGYQPNYHAVNIVGYSN	179	
Db	121	SPDPSNKIROALQTHTAFAVIIGIKDLNAPRHYDGRITMQHDNGYQPNYHAVNIVGYN	180	
Qy	180	AQGVYDVIVRNSWDTNWGNDNGYGYFAANIDL 210		
Db	181	TQGVYDVIVRNSWDTTWGNDNGYGYFAANINL 211		

RESULT 2

S03380
major fecal allergen Der p 1 - house-dust mite (Dermatophagoides pteronyssinus) (fragment)
N;Alternate names: allergen Der p1
C;Species: Dermatophagoides pteronyssinus
C;Date: 05-Mar-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S03380
R;Simpson, R.J.; Nice, E.C.; Moritz, R.L.; Stewart, G.A.
Protein Seq. Data Anal. 2, 17-21, 1989
A;Title: Structural studies on the allergen Der p1 from the house dust mite Dermatophago
A;Reference number: A31657; MUID:89098855; PMID:2911558

Dd 178 KKYIWNKSWGKGWGDGYITPWADRNKHCGGIATAASYPLV 218

RESULT 7
A59040
Cysteine proteinase I (EC 3.4.22.-) - ginger
C;Species: Zingiber officinale [ginger]
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: A59040
R;Laursen, R.A.
submitted to: The Protein Sequence Database, July 1999
A;Description: Amino acid sequences of cysteine proteases from ginger rhizome
A;Reference number: A59040
A;Accession: A59040
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-221 <LAU>
A;Cross-references: UNIPROT:P82473
A;Experimental source: rhizome
A;Note: residues 80-87 were not determined but are based on mass measurement
C;Superfamily: papain
F;Keywords: cysteine proteinase; glycoprotein; hydrolase
F;24-65,59-98,155-206/Disulfide bonds: #status predicted
F;27,161,181/Active site: Cys, His, Asn #status predicted
F;95,156/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.5%; Score 295; DB 2; Length 221;
Best Local Similarity 32.0%; Pred. No.3.8e-19;
Matches 65; Conservative 35; Mismatches 91; Indels 12; Gaps

Qy 11 PAEIDLQRMTVTPIRMGGCCGCSCWAISGVAAATESAYLARNOSGLDAEQELVDCAQS-Q-H
Db 4 PDSIDWRKEGAVPVYKNQGCGCSGWAFDATAAASVGINQIVTGDILSLEQQLVDCSTRNH
Qy 70 GGCHGTDPGRITYIOHN-GVVQESYRYVAREQC-SRPNAQRFGISNYCOIYPNPANKI
Db 64 GECEGPFRATPQTIIINNNGINSSEHPYTGNCTCKENAHVVSIDSIRNVPSNDEKS-L
Qy 128 REALAQTHSAIAVIIGIKDLDFRRH--YDGRTIIQRDNGYQPNNYHAVNI VGSNAOQVDY
Db 124 QXAVANQPVSVMTDAGRFQLYENGIFTGSCNISAN-----HYRTVGRETENDKD-Y
Qy 186 WTVRNSWDTNMGDNQYGYYFAANI 208
Db 177 WTVKNSWGKNMGSGYIRVERNI 199

RESULT 8
S15844
cathepsin S (EC 3.4.22.27) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 12-Feb-1993 #sequence revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: S15844; S23680; S16972; S23957
R;Kitonja, A.; Colic, A.; Dolenc, I.; Ogrinc, T.; Podobnik, M.; Turk, V.
FEBS Lett. 283, 329-331, 1991
A;Title: The complete amino acid sequence of bovine cathepsin S and a partial cDNA clone
A;Reference number: S15844; MUID:91257334; PMID:2044774
A;Accession: S15844
A;Molecule type: protein
A;Residues: 1-217 <KIT>
A;Cross-references: UNIPROT:P25326
R;Wiederanders, B.; Broemme, D.; Kirschke, H.; Kalkkinen, N.; Rinne, A.; Paasinen,
FEBS Lett. 286, 189-192, 1991
A;Title: Primary structure of bovine cathepsin S. Comparison to cathepsins L and F
A;Reference number: S16972; MUID:91323515; PMID:1864368
A;Accession: S23680
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 22-217 <WIE>
A;Cross-references: GB:M95211; NID:g162814; PIDN:AAA30435.1; PID:g162815
A;Note: 143-Pro was also found
A;Accession: S16972
A;Molecule type: protein

A;Residues: 1-28;48-71;94-104;107-131;146-162;178-217 <W12>
C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase
F;12-110;22-66;56-99;158-206/Disulfide bonds: #status predicted
F;25;164;184/Active site: Cys, His, Asn #status predicted

Query Match 23.6%; Score 284.5; DB 2; Length 217;
Best Local Similarity 33.8%; Pred. No. 3.2e-18;
Matches 69; Conservative 33; Mismatches 91; Indels 11; Gaps 6;

QY 11 PAEIDLQRMRTVTPIRMQCGSCGSAFSGVAATESAYLAHRNOSLDLAEQELVDCAS--- 67
DQ 2 PDSMDWRKCGVTEVYQAGCGSCGSAFSAVGALEAQVGLKGTGLVLSLAQNLVDCSTAKY 61
QY 68 -QHCHGDTTIPRGIEY-IQHNGVVQSYRYVAREOSCRPNRQRFG-ISNYCQIYPPNA 124
DQ 62 GNKGCGGFFTEAFQVIIDNNGIDSEASYPKAMDGKQYDVKNRAATCSRYIELPFGSE 121
QY 125 NKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQDNGYQPNY-HAVNIVGYSNAQGV 183
DQ 122 EALKEAVANKG---PVSVGI-DASHSSFFLYKTCVYDPSCTQNVHGVLVVGYGNLDGK 177
QY 184 DYWIVRNSWDTNWDNGYGYFAAN 207
DQ 178 DYWLKNSWGLHFGDQGYRMARN 201

RESULT 9

S46476
cysteine proteinase (EC 3.4.22.-) III - mountain papaya
C;Species: Carica pubescens (mountain papaya)
C;Date: 15-Jul-1995 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
C;Accession: S46476; S35579
R;Jaziri, M.; Kleinschmidt, T.; Walraevens, V.; Schneek, A.G.; Looze, Y.
Biol. Chem. Hoppe-Seyler 375, 379-385, 1994
A;Title: Primary structure of CC-III, the glycosylated cysteine proteinase from the late
A;Reference number: S46476; MUID:95071624; PMID:7980869
A;Accession: S46476
A;Molecule type: protein
A;Residues: 1-214 <JAZ>
R;Walraevens, V.; Jaziri, M.; van Beeumen, J.; Schneek, A.G.; Kleinschmidt, T.; Looze, Y.
Biol. Chem. Hoppe-Seyler 374, 501-506, 1993
A;Title: Isolation and preliminary characterization of the cysteine-proteinases from the
A;Reference number: S35577; MUID:94030669; PMID:8216902
A;Accession: S35579
A;Molecule type: protein
A;Residues: 1-21, 'X', 23-24, 'X', 26-43 <WAL>
A;Note: the source is designated as Carica candamarcensis
C;Superfamily: papain
C;Keywords: cysteine proteinase; glycoprotein; hydrolase
F;1-214/Product: cysteine proteinase III #status experimental <MAT>
F;22-63;56-95;153-200/Disulfide bonds: #status predicted
F;25;159;175/Active site: Cys, His, Asn #status predicted
F;44/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 22.7%; Score 274; DB 2; Length 214;
Best Local Similarity 35.9%; Pred. No. 2.8e-17;
Matches 70; Conservative 33; Mismatches 79; Indels 14; Gaps 9;

QY 11 PAEIDLQRMRTVTPIRMQCGSCGSAFSGVAATESA-YLAHRNOSLDLAEQELVDC-ASQ 68
DQ 2 PESIDWRKCGAVTPVKNQCGSCGSAFSTIATVEGINKIVHGLT-SLSQELVDCRRS 60
QY 69 HGCHGDTTIPRGIEYIQHNGVVQSYRYVAREOSCRPNRQRF--FGISNYCQIYPPNANK 126
DQ 61 HGCKGGYQTTSLKYVDVHDGVTKEYPYEEKQYKCRADKKPKVPIKISGKYK--PSNDE 118
QY 127 IREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQDNGYQPNYHVNIVGYSNAQGV 186
DQ 119 ISLIKATKQPVSVLVESKG-KAFQFYK-KGIFGPGCTKVD-HAVTAVGY----GKDYI 171
QY 187 IVRNSWDTNWDNGY 201

Db 172 LIKNSWGPXWGXGY 186

RESULT 10

S67481
cathepsin L-like cysteine proteinase (EC 3.4.22.-) CPl [similarity] - fruit fly (Drosophila)
C;Species: Drosophila melanogaster
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Apr-2000
C;Accession: S67481
R;Matsumoto, I.; Watanabe, H.; Abe, K.; Arai, S.; Emori, Y.
Eur. J. Biochem. 227, 582-587, 1995
A;Title: A putative digestive cysteine proteinase from Drosophila melanogaster is predominant
A;Reference number: S67481; MUID:95154345; PMID:7851441
A;Accession: S67481
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <MAT>
A;Cross-references: EMBL:D31970
A;Note: the authors translated the codon CCT for residue 126 as Ala and CCC for residue 1
C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase
F;25;164;185/Active site: Cys, His, Asn #status predicted

Query Match 22.6%; Score 273; DB 2; Length 218;
Best Local Similarity 32.7%; Pred. No. 3.5e-17;
Matches 64; Conservative 28; Mismatches 98; Indels 6; Gaps 4;

QY 11 PAEIDLQRMRTVTPIRMQCGSCGSAFSGVAATESAYLAHRNOSLDLAEQELVDCASQH- 69
DQ 2 PKSVDRWRTKGAVTAVKQDQHGCGSCGSAFSGTGALEQHFPRKSGVLVLSQNLVDCSTKYG 61
QY 70 --GCHGDTTIPRGIEYIQHNGVVQ--ESYRYVAREOSCRPNRQRFSGISNYCQIYPPNANK 126
DQ 62 NNGCNGGLMDNAPPYIKNGGIDTEKSYEYEAIDDSCHFNRAQVGTADRGFTDPOGDEK 121
QY 127 IREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQDNGYQPNYHVNIVGYSNAQGV 185
DQ 122 KMPEPVPTVGPVSVAIDASH-ESFQYSEGVNPEQCDALNDHGLVVGFGTDESGEDY 180
QY 186 WIVRNSWDTNWDNGY 201
DQ 181 WLKNSWGTWGDGKF 196

RESULT 11

S03964
stem bromelain (EC 3.4.22.32) - pineapple
C;Species: Ananas comosus (pineapple)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S03964
R;Ritonja, A.; Rowan, A.D.; Buttle, D.J.; Rawlings, N.D.; Turk, V.; Barrett, A.J.
FEBS Lett. 247, 419-424, 1989
A;Title: Stem bromelain: amino acid sequence and implications for weak binding of cystatins
A;Reference number: S03964; MUID:89232167; PMID:2714443
A;Accession: S03964
A;Molecule type: protein
A;Residues: 1-212 <RIT>
A;Cross-references: UNIPROT:P14518
C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase

Query Match 19.9%; Score 240; DB 2; Length 212;
Best Local Similarity 31.2%; Pred. No. 3.2e-14;
Matches 63; Conservative 32; Mismatches 91; Indels 16; Gaps 6;

QY 11 PAEIDLQRMRTVTPIRMQCGSCGSAFSGVAATESAYLAHRNOSLDLAEQELVDCASQHG 70
DQ 3 PQSIDWRDYGAVTSVKNQPCGACWAFAAIATVTSYIKIKKGLLEPLSEQQVLDCAKGYG 62
QY 71 CHGDTTIPRGIEYIQHNGVVQSYRYVAREOSCR--PNAORFGISNYCQIYPPNANK 126
DQ 63 CKGGWEFRAPEFTISNKGVASGAIPYKAAKGTCTDGVPSNAY--ITGYARVPRNNESS 120

```

QY 127 IREALAQTHSAIAVIIGIKDLDFRHYDG-----RTIQRDNGYQPNYHAVNIVGYSN 179
      ||:  :::  |||:  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 61 WALQTAVTYQVSVVALDAAG-DAFKHYSGIGFTGPGCTAID-----HAVTIVGYGT 110

QY 180 AQGVDTWIVNSWDTWGNDGYGYFAANI 208
      ||:  ||:  |||:  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 111 EGGIDYWIIVKNSWDTTWGEGYMRILRN 139

RESULT 14
B44938
cysteine proteinase (EC 3.4.22.-) - Trypanosoma brucei (fragment)
C/Species: Trypanosoma brucei
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: B44938
R/Eakin, A.E.; Bouvier, J.; Sakanari, J.A.; Craik, C.S.; McKerrow, J.H.
Mol. Biochem. Parasitol. 39, 1-8, 1990
A/Title: Amplification and sequencing of genomic DNA fragments encoding cysteine
A/Reference number: A44938; MUID:90158686; PMID:2406590
A/Accession: B44938
A/Status: preliminary; nucleic acid sequence not shown; not compared with concen
A/Molecule type: DNA
A/Residues: 1-166 <EAK>
A/Cross-references: UNIPROT:Q26742; GB:M27306
C/Superfamily: papain
C/Keywords: cysteine proteinase; hydrolase

Query Match 15.4%; Score 185.5; DB 2; Length 166;
Best Local Similarity 33.5%; Pred. No. 1.9e-09;
Matches 59; Conservative 25; Mismatches 75; Indels 15; Gaps 8;

QY 28 QCGCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVDCASQHGCHGDTIPRGIEYI-OHN 86
      ||:  |||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:
Db 1 QCGCGSCWAFSTIGNIEGQWQVAGNPLVLSLEQLIYVCDPLIGCGGLMDNPFNWIIVNSN 60

QY 87 G--VVOESYRYVA--REQSCRPNARFG--ISNYCQIYPPNANKIREALAOHSA-AIA 139
      ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:
Db 61 GGNVFTSEASYPYVSGNGEQPQCQMGNGHEIGAAITDHDVL-PQDEDAIAAYLAENRPLAIA 119

QY 140 VIIGIKDLDFRHYDGRITIQRDNGYQPNYHAVNIVGYSNAQGVDTWIVNSW 192
      ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:
Db 120 V-----EAPQFYGHNGGYILTCTSEQLD-HGVLLVGYNDNSPPYWIIVNSW 166

RESULT 15
PQ0650
senescence-associated protein SAG2 - Arabidopsis thaliana (fragment)
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C/Accession: PQ0650
R/Hensel, L.L.; Grbic, V.; Baumgarten, D.A.; Blecker, A.B.
Plant Cell 5, 553-564, 1993
A/Title: Developmental and age-related processes that influence the longevity a
A/Reference number: PQ0650; MUID:93299122; PMID:8518555
A/Accession: PQ0650
A/Molecule type: mRNA
A/Residues: 1-95 <HEN>
A/Cross-references: UNIPROT:Q9LL83
C/Comment: This protein is a senescence-associated protein.
C/Genetics:
A/Gene: SAG2
C/Superfamily: papain

Query Match 14.8%; Score 179; DB 2; Length 95;
Best Local Similarity 42.2%; Pred. No. 3.8e-09;
Matches 38; Conservative 15; Mismatches 33; Indels 4; Gaps 2;

QY 11 PAEIDLQRMETVPIRMQCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVDCA---S 67
      ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:  ||:
Db 6 PETKQWREDGIVSPKDDQCGCGSCWTFSTTTGALEAAHYQAFGKISLSEQQLVDCAGAFN 65

QY 68 OHGCHGDTIPRGIEYIQHNGVVO-ESYRY 96

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:35:53 ; Search time 175 Seconds
(without alignments)
649.609 Million cell updates/sec

Title: US-09-867-159A-2

Perfect score: 1206

Sequence: 1 TNACSSINGNAPAEIDLQMR.....YFAANIDLMMEIEPPYVIL 222

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 737793

Minimum DB seq length: 0

Maximum DB seq length: 222

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.4

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	944.5	78.3	210	2 Q9GY0	Q9GY0 dermatophag
2	607	50.3	146	2 Q95X05	Q95X05 dermatophag
3	469	38.9	107	2 Q95X04	Q95X04 dermatophag
4	437	36.2	133	2 Q968Y3	Q968Y3 dermatophag
5	389.5	32.3	94	2 Q7M431	Q7M431 dermatophag
6	382	31.7	221	2 Q95P34	Q95P34 blomia trop
7	315	26.1	215	1 ERVB_TABDI	P60994 tabernaemon
8	313.5	26.0	219	2 Q9NGW1	Q9NGW1 fasciola gi
9	311	25.8	221	1 GPII_ZINOF	P82474 zingiber of
10	300	24.9	218	1 CATL_CHICK	P09648 gallus gall
11	295	24.5	213	1 MDOL_PSEMR	P83443 pseudananas
12	295	24.5	221	1 GPI_ZINOF	P82473 zingiber of
13	291	24.1	214	2 Q6WSH4	Q6WSH4 ancylostoma
14	286	23.7	208	1 ERVC_TABDI	P83654 tabernaemon
15	284.5	23.6	217	1 CATS_BOVIN	P25326 bos taurus
16	279	23.1	178	2 Q9SDN1	Q9SDN1 prunus dulc
17	276	22.9	215	2 Q6TXV9	Q6TXV9 glycine max
18	276	22.9	216	2 Q26559	Q26559 spirometra
19	275.5	22.8	219	2 Q9NGW0	Q9NGW0 fasciola gi
20	267	22.1	189	2 Q966T7	Q966T7 spirometra
21	266.5	22.1	181	2 Q9NH98	Q9NH98 stylonychia
22	265.5	22.0	189	2 Q8T8B8	Q8T8B8 halichondri
23	258	21.4	196	2 Q8I889	Q8I889 leptinotars
24	257	21.3	222	2 Q868H3	Q868H3 leishmania
25	253.5	21.0	166	2 Q24943	Q24943 fasciola he
26	249.5	20.7	171	1 CATL_SHEEP	Q10991 ovis aries
27	248.5	20.6	166	2 Q24942	Q24942 fasciola he
28	241	20.0	196	2 Q8I888	Q8I888 leptinotars
29	240	19.9	212	1 BROW_ANACO	P14518 ananas como
30	239.5	19.9	166	2 Q24945	Q24945 fasciola he
31	238.5	19.8	189	2 Q9NHV3	Q9NHV3 babesia equ

32	237.5	19.7	176	2	Q94C46	Q94C46 carica cand
33	236.5	19.6	167	2	Q8I881	Q8I881 leptinotars
34	232.5	19.3	181	2	Q84XA1	Q84XA1 carica cand
35	231	19.2	217	2	Q9U0C5	Q9U0C5 clonorchie
36	230	19.1	166	2	Q6LAF8	Q6LAF8 homo sapien
37	228.5	18.9	191	2	Q6JZ26	Q6JZ26 fundulus he
38	227.5	18.9	177	2	Q70B20	Q70B20 platichthys
39	226.5	18.8	166	2	Q24948	Q24948 fasciola he
40	223	18.5	175	2	Q6LAF7	Q6LAF7 homo sapien
41	222.5	18.4	168	2	Q43947	Q43947 sarcocystis
42	220	18.2	174	2	Q868H2	Q868H2 leishmania
43	219.5	18.2	163	2	Q9SPU9	Q9SPU9 hordeum vul
44	218.5	18.1	166	2	Q24946	Q24946 fasciola he
45	214	17.7	165	2	Q8T4J2	Q8T4J2 pagumogonim

ALIGNMENTS

RESULT 1						
ID	Q9GY0	PRELIMINARY;	PRT;	210 AA.		
AC	Q9GY0;					
DT	01-MAR-2001	(TremBLrel. 16, Created)				
DT	01-MAR-2001	(TremBLrel. 16, last sequence update)				
DT	01-MAR-2004	(TremBLrel. 26, last annotation update)				
DE	Allergen Der f1 (Fragment).					
OS	Dermatophagoides farinae (House-dust mite).					
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;					
OC	Acariformes; Sarcotiformes; Astigmata; Psoroptidia; Analgoidea;					
OC	Pyroglyphidae; Dermatophagoides.					
OX	NCBI_TaxID=6954;					
RP	[1]					
RP	SEQUENCE FROM N.A.					
RA	Hao M.O., Xu J., Zhong N.S.;					
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.					
CC	-/- SIMILARITY: Belongs to peptidase family C1.					
DR	EMBL; AF285763; AAG00520.1; -					
DR	PIR; A27634; A27634.					
DR	HSSP; P80067; IJQP.					
DR	GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.					
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.					
DR	InterPro; IPR000668; Peptidase_C1.					
DR	Pfam; PF00112; Peptidase_C1; 1.					
DR	PRINTS; PR00705; PAPAIN.					
DR	SMART; SM00645; Pept C1; 1.					
DR	PROSITE; PS00640; THIOL_PROTEASE ASN; 1.					
DR	PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.					
DR	PROSITE; PS00639; THIOL_PROTEASE HIS; UNKNOWN_1.					
KW	Hydrolase; Protease; Thiol protease.					
FT	NON_TER 1					
FT	NON_TER 210					
SQ	SEQUENCE 210 AA; 23548 MW; EA08029D642EEB90 CRC64;					
Query Match 78.3%; Score 944.5; DB 2; Length 210;						
Best Local Similarity 81.4%; Pred. No. 1.1e-76;						
Matches 171; Conservative 16; Mismatches 22; Indels 1; Gaps 1;						
QY	2	NACSSING-NAPAEIDLQMRVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ				
DB	1	SACRINSVNPSELDLSRLTPTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLSEQ				
QY	61	ELVDCASOHCHGDTIPRGLEYIQHNGVQESYRYVAREQSCRRPNAQRFGINSYCQIY				
DB	61	ELVDCASOHCHGDTIPRGLEYIQHNGVQESYRYVAREQSCRRPNSQHYGISN				
QY	121	PPNANKIREALAOQTHSAIAVIIGIKDLDAFRHYDGRITIIQDNGYQPNYHVNIVGYSNA				
DB	121	PPDVQKIREALTQHTAIAVIIGIKDLRAFOHYDGRITIIQDNGYQPNYHVNIVGYSNA				
QY	181	QGVYDIWIVRNSWDTNWGDNGYGYFAANIDL 210				

Db 181 QGVYVIVRNSWDTTWGDSGYFQAGNNL 210

Query Match 38.9%; Score 469; DB 2; Length 107;
 Best Local Similarity 80.4%; Pred. No. 2.5e-34;
 Matches 86; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

RESULT 2

Q95X05 ID Q95X05 PRELIMINARY; PRT; 146 AA.

AC Q95X05; DB 1 QGVYVIVRNSWDTTWGDSGYFQAGNNL 210

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Cysteine proteinase (Fragment).

DE Name=CPW2;

OS Dermatophagoides farinae (House-dust mite).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

OC Acariformes; Sarcophagales; Astigmata; Psoroptidia; Analgoidea;

OC Pyroglyphidae; Dermatophagoides.

OC NCBI_TaxID=6954;

OX [1]

RP SEQUENCE FROM N.A.

RA Park H., Park S.Y., Kim K.Y., Yun H.C.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RL EMBL: AF194431; AAL14424.1; -

DR HSP; P43235; 18Y8.

DR GO: GO:0008234; F:cysteine-type peptidase activity; IEA.

DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro: IPR000668; Peptidase_C1.

DR Pfam: PF00112; Peptidase_C1; 1.

DR NON_TER 1

FT NON_TER 146

FT NON_TER 146

SQ SEQUENCE 146 AA; 16852 MW; BB304800946D4047 CRC64;

Query Match 50.3%; Score 607; DB 2; Length 146;
 Best Local Similarity 84.2%; Pred. No. 1.5e-46;
 Matches 112; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Q95X05 ID Q95X05 PRELIMINARY; PRT; 107 AA.

AC Q95X05; DB 1 QGVYVIVRNSWDTTWGDSGYFQAGNNL 210

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Cysteine proteinase (fragment).

DE Name=CPW3;

OS Dermatophagoides farinae (House-dust mite).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

OC Acariformes; Sarcophagales; Astigmata; Psoroptidia; Analgoidea;

OC Pyroglyphidae; Dermatophagoides.

OC NCBI_TaxID=6954;

OX [1]

RP SEQUENCE FROM N.A.

RA Park H., Park S.Y., Kim K.Y., Yun H.C.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RL EMBL: AF194432; AAL14425.1; -

DR HSP; P43235; 18Y8.

DR GO: GO:0008234; F:cysteine-type peptidase activity; IEA.

DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro: IPR000668; Peptidase_C1.

DR Pfam: PF00112; Peptidase_C1; 1.

DR NON_TER 1

FT NON_TER 107

FT NON_TER 107

SQ SEQUENCE 107 AA; 12277 MW; A80E7876CBA6F97A CRC64;

Query Match 36.2%; Score 437; DB 2; Length 133;
 Best Local Similarity 61.4%; Pred. No. 2.4e-31;
 Matches 81; Conservative 17; Mismatches 34; Indels 0; Gaps 0;

Q95X04 ID Q95X04 PRELIMINARY; PRT; 107 AA.

AC Q95X04; DB 1 QGVYVIVRNSWDTTWGDSGYFQAGNNL 210

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Cysteine proteinase (fragment).

DE Name=CPW3;

OS Dermatophagoides farinae (House-dust mite).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

OC Acariformes; Sarcophagales; Astigmata; Psoroptidia; Analgoidea;

OC Pyroglyphidae; Dermatophagoides.

OC NCBI_TaxID=6954;

OX [1]

RP SEQUENCE FROM N.A.

RA Park H., Park S.Y., Kim K.Y., Yun H.C.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RL EMBL: AF194432; AAL14425.1; -

DR HSP; P43235; 18Y8.

DR GO: GO:0008234; F:cysteine-type peptidase activity; IEA.

DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro: IPR000668; Peptidase_C1.

DR Pfam: PF00112; Peptidase_C1; 1.

DR NON_TER 1

FT NON_TER 107

FT NON_TER 107

SQ SEQUENCE 107 AA; 12277 MW; A80E7876CBA6F97A CRC64;

Query Match 36.2%; Score 437; DB 2; Length 133;
 Best Local Similarity 61.4%; Pred. No. 2.4e-31;
 Matches 81; Conservative 17; Mismatches 34; Indels 0; Gaps 0;

Q95X04 ID Q95X04 PRELIMINARY; PRT; 107 AA.

AC Q95X04; DB 1 QGVYVIVRNSWDTTWGDSGYFQAGNNL 210

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Cysteine proteinase (fragment).

DE Name=CPW3;

OS Dermatophagoides farinae (House-dust mite).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

OC Acariformes; Sarcophagales; Astigmata; Psoroptidia; Analgoidea;

OC Pyroglyphidae; Dermatophagoides.

OC NCBI_TaxID=6954;

OX [1]

RP SEQUENCE FROM N.A.

RA Park H., Park S.Y., Kim K.Y., Yun H.C.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RL EMBL: AF194432; AAL14425.1; -

DR HSP; P43235; 18Y8.

DR GO: GO:0008234; F:cysteine-type peptidase activity; IEA.

DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro: IPR000668; Peptidase_C1.

DR Pfam: PF00112; Peptidase_C1; 1.

DR NON_TER 1

FT NON_TER 107

FT NON_TER 107

SQ SEQUENCE 107 AA; 12277 MW; A80E7876CBA6F97A CRC64;

Query Match 36.2%; Score 437; DB 2; Length 133;
 Best Local Similarity 61.4%; Pred. No. 2.4e-31;
 Matches 81; Conservative 17; Mismatches 34; Indels 0; Gaps 0;

Q95X04 ID Q95X04 PRELIMINARY; PRT; 107 AA.

AC Q95X04; DB 1 QGVYVIVRNSWDTTWGDSGYFQAGNNL 210

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Cysteine proteinase (fragment).

DE Name=CPW3;

OS Dermatophagoides farinae (House-dust mite).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

OC Acariformes; Sarcophagales; Astigmata; Psoroptidia; Analgoidea;

OC Pyroglyphidae; Dermatophagoides.

OC NCBI_TaxID=6954;

OX [1]

RP SEQUENCE FROM N.A.

RA Park H., Park S.Y., Kim K.Y., Yun H.C.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RL EMBL: AF194432; AAL14425.1; -

DR HSP; P43235; 18Y8.

DR GO: GO:0008234; F:cysteine-type peptidase activity; IEA.

DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro: IPR000668; Peptidase_C1.

DR Pfam: PF00112; Peptidase_C1; 1.

DR NON_TER 1

FT NON_TER 107

FT NON_TER 107

SQ SEQUENCE 107 AA; 12277 MW; A80E7876CBA6F97A CRC64;

Query Match 36.2%; Score 437; DB 2; Length 133;
 Best Local Similarity 61.4%; Pred. No. 2.4e-31;
 Matches 81; Conservative 17; Mismatches 34; Indels 0; Gaps 0;

Q95X04 ID Q95X04 PRELIMINARY; PRT; 107 AA.

AC Q95X04; DB 1 QGVYVIVRNSWDTTWGDSGYFQAGNNL 210

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Cysteine proteinase (fragment).

DE Name=CPW3;

OS Dermatophagoides farinae (House-dust mite).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

OC Acariformes; Sarcophagales; Astigmata; Psoroptidia; Analgoidea;

OC Pyroglyphidae; Dermatophagoides.

OC NCBI_TaxID=6954;

OX [1]

RP SEQUENCE FROM N.A.

RA Park H., Park S.Y., Kim K.Y., Yun H.C.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RL EMBL: AF194432; AAL14425.1; -

DR

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RX MEDLINE=89098855; PubMed=2911558;
RA Simpson R.J., Nice E.C., Moritz R.L., Stewart G.A.;
RT "Structural studies on the allergen Der p1 from the house dust mite
RT Dermatophagoides pteronyssinus: similarity with cysteine
RL proteinases.";
DR Protein Seq. Data Anal. 2:17-21(1989).
DR PIR; S03380; S03380.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000668; Peptidase_C1.
DR ProDom; PD000158; Peptidase_C1; 1.
FT NON_TER 1 94
FT SEQUENCE 94 AA; 10327 MW; 9BF744165C8428A8 CRC64;

Query Match 32.3%; Score 389.5; DB 2; Length 94;
Best Local Similarity 48.6%; Pred. No. 2.9e-27;
Matches 88; Conservative 0; Mismatches 4; Indels 89; Gaps 4;

QY 1 TNACISNGNAPAEIDLQMRVTVPPIR--MQGGCGSCWAFSGVAATESAYLAHRNQSLLDLA 58
Db 1 TNACISNGNAPAEIDLQMRVTVPPIRQMGGCGSGXXAFSGVA----- 43
QY 59 EQELVDCASQHGCHDTPRGIEYIOHNGVVOESYRYRVAREQSCRPNACQ--RFGISNYCQ 120
Db 44 -----GIEYIOHNGVVOESY-----RFGISNYCQ 68
QY 119 IYPNANKIREALQTHSAIAVIIGIKDLDA-FRHYDGRITFIQRDNGYQPNYHVNIGYS 178
Db 69 IYPNANK-----DNGYQPNYHVNIGYX 93
QY 179 N 179
Db 94 N 94

RESULT 6
ID Q95PJ4 PRELIMINARY; PRT; 221 AA.
AC Q95PJ4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Cysteine protease (Fragment).
OS Blomia tropicalis (Mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptiformes; Astigmata; Glycyphagoidea;
OC Echinopodidae; Blomia.
OX NCBI_TaxID=40697;
RN [1]
RP SEQUENCE FROM N.A.
RA Mora C.I., Diaz A.M., Montealegre F., Flores I.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF277840; AAK58415.1; -.
DR HSP; P53634; I1K3B.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; Pept_cys_acsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR SMART; SM00645; Pept C1; 1.
DR PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; UNKNOWN_1.
KW Protease.
FT NON_TER 1 221
FT CHAIN <1 221 cysteine protease.
SQ SEQUENCE 221 AA; 25126 MW; 272B45EA53F2900 CRC64;

Query Match 31.7%; Score 382; DB 2; Length 221;
Best Local Similarity 38.4%; Pred. No. 3.7e-26;
Matches 86; Conservative 35; Mismatches 77; Indels 26; Gaps 8;

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QY 11 PAEIDLQMRVTVPPIRQMGGCGSCWAFSGVAATESAYLAHRNQSLLDLAEOELVDCASQ-- 68
Db 2 PANFDRQKTHVNPPIRQMGGCGSCWAFSGVAATESAYLAHRNQSLLDLCTHYLY 61
QY 69 -----HGCHGDTIPRGIEYIOHNGVVOESYRYRVAREQSCRPNACQ--RFGISNYCQ 120
Db 62 DPTVKHGCOSGMSPEAFKTKMKQKLESHYPYMKLNQC-QANVAGTRTHVSY----- 116
QY 121 PNANKIREALQTHSAI-----AVIIGIKDLDA-FRHYDGRITFIQRDNGYQPNY--HAVN 173
Db 117 --NSLRYRAGDQETQAAIMNHGPPVVIYHGTAEHFRNL--RKGLRGAGYNDQIDHAVV 172
QY 174 IVGYSNAQGVYDVIWRNSWTNWDNGYGYFAANIDLMIEEYP 217
Db 173 LVGMGTQNGIDYIVRTISWGTQMGDAGYGFVERHNSLGINNY 216

RESULT 7
ERVB TABDI STANDARD; PRT; 215 AA.
AC P60994;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ervatom B (EC 3.4.22.-) (ERV-B).
OS Tabernaemontana divaricata (Crepe jasmine) (Ervatamia coronaria).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamids; Gentianales; Apocynaceae; Rauvolfioideae; Tabernmontaneae;
OC Tabernaemontana.
OX NCBI_TaxID=52861;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RA Biswas S., Chakrabarti C., Kundu S., Jagannadham M.V.,
RA Dattagupta J.K.;
RT "Proposed amino acid sequence and the 1.63 A X-ray crystal structure
RT of a plant cysteine protease, ervatamin B: some insights into the
RT structural basis of its stability and substrate specificity.";
RL Proteins 51:489-497(2003).
RN [2]
RP SEQUENCE OF 1-21, AND CHARACTERIZATION.
RC TISSUE=Latex;
RX PubMed=10691612; DOI=10.1021/jf990661j;
RA Kundu S., Sundd M., Jagannadham M.V.;
RT "Purification and characterization of a stable cysteine protease
RT ervatamin B, with two disulfide bridges, from the latex of Ervatamia
RT coronaria.";
RL J. Agric. Food Chem. 48:171-179(2000).
CC -!- FUNCTION: Cysteine protease.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Laticifer.
CC -!- PTM: Not glycosylated.
CC -!- MISCELLANEOUS: Active over the pH range 3.0-10.5 and up to 62
CC degrees Celsius. Stable in 8 M urea and 2.5 M GuHCl at neutral pH,
CC in 40% acetonitrile, 70% ethanol and 50% methanol. Unstable in
CC SDS.
CC -!- SIMILARITY: Belongs to the peptidase C1 family.
DR PIR; A59428; A59428.
DR PDB; 1LWD; X-ray; A=1-215.
DR MEROPS; C01.099; -.
DR ProDom; PD000158; Peptidase C1; 1.
DR PROSITE; PS00640; THIOI_PROTEASE ASN; 1.
DR PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; FALSE NEG.
KW 3D-structure; Direct protein sequencing; Hydrolase; Thiol protease.
FT ACT_SITE 25 25
FT ACT_SITE 158 158 By similarity.
FT ACT_SITE 178 178
FT DISULFID 22 63
FT DISULFID 56 96
FT DISULFID 152 203
SQ SEQUENCE 215 AA; 23183 MW; 4DE62E43BA4F4F83 CRC64;

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Query Match      26.1%; Score 315; DB 1; Length 215;
Best Local Similarity 34.5%; Pred. No. 3.7e-20;
Matches 76; Conservative 32; Mismatches 90; Indels 22; Gaps 7;

QY 11 PABIDLRQMTVTPIRMQCGSCGSCWAFSGVAATESAYLAHRNQLDLAQELVDC-ASQH 69
Db 2 PSFVDRSKGAVNSIKNQCGSCWAFSAVAVESINKRTGQLISLSEQLVDCDTASH 61
QY 70 GCHGDTIPRGIEVIQNVVQ-BSYRYVAREOSCRPNQAQREGISYQIYPPNANKIR 128
Db 62 GCGGWMNAFQYIITNGGIDTQONTQYPSAVQSGCKPYRLRVVVSINGFORVTRNNEALSQ 121
QY 129 EALAQTHSALAVIIGIKDLDA----FRHYDGRITIIQDNGYQPNYHVNIVGYSNAQGV 184
Db 122 SAVASQPVSVTV-----EACAPQHYSS-GIFTGPGCTAQN-HGVIVIGYGTOSGKN 172
QY 185 YWTVRNSWDTNMGDNGYGYFAANI-----DLMMIEEYP 217
Db 173 YWTVRNSWGNQGNQGYIMWERNVASSAGLCGIAQLPSYP 212

RESULT 8
Q9NGW1 PRELIMINARY; PRT; 219 AA.
AC Q9NGW1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cathepsin L (Fragment).
GN Namescat-L1E;
OS Fasciola gigantica (Giant liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fascioloidae; Fasciolidae; Fasciola.
OX NCBI_TaxID=46835;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21332182; PubMed=11438432; DOI=10.1016/S1383-5769(01)00068-X;
RA Grams R., Vichasari-Grams S., Sobhon P., Upatham E.S., Viyanant V.;
RT "Molecular cloning and characterization of cathepsin L encoding genes
from Fasciola gigantica."
RL Parasitol. Int. 50:105-114(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Grams S.V., Grams R., Sobhon P., Viyanant V., Upatham E.S.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family C1.
DR EMBL; AF239267; AAP44678.1; -.
DR HSSP; P53634; 1K3B.
DR MEROPS; C01.033; -.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; Pept_cys_acsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR SMART; SM00645; Pept C1; 1.
DR PROSITE; PS00640; THIOI_PROTEASE_ASN; 1.
DR PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; 1.
KW Hydrolase; Protease; Thiol protease.
FT NON_TER 1
SQ SEQUENCE 219 AA; 24217 MW; 7F443104B4071D3C CRC64;

Query Match      26.0%; Score 313.5; DB 2; Length 219;
Best Local Similarity 32.4%; Pred. No. 5.2e-20;
Matches 73; Conservative 39; Mismatches 88; Indels 25; Gaps 7;

QY 11 PABIDLRQMTVTPIRMQCGSCGSCWAFSGVAATESAYLAHRNQLDLAQELVDC-AS 67
Db 2 PDKIDRESGYTEVDKQKCGSCWAFSTGTGTGWTMKNERTSISFSEQLVDCSGPWG 61
QY 68 QHGHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNQAQREGISYQIYPPNA 124

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Db 62 NYGCMGGLMENAYEYLKQFGLTESYPYTAVEDQCR--YNRLGVAKYTDYTVHSGSE 119
QY 125 NKIREAL-AQTHSAIAVIIGIKDLDA-FRHYDGRITIIQDNGYQPNYHVNIVGYSNAQ 182
Db 120 VELKNLVGAEGPAAVAV-----DVSEDFMWSGGIYQSRSTCSSLRVNHAVLAVGYGTGG 174
QY 183 VDYWTVRNSWDTNMGDNGYGYFAAN-----IDLMMIEEYP 217
Db 175 TDWTVRNSWGSWGSGRGYIRVWRNKGNGMGCIASLASLPVAFPP 219

RESULT 9
GPII_ZINOF
ID GPII_ZINOF STANDARD; PRT; 221 AA.
AC P82474;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cysteine proteinase GP-II (EC 3.4.22.-).
OS Zingiber officinale (Ginger).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Zingiberaceae;
OC Zingiber.
OX NCBI_TaxID=94328;
RN [1]
RP SEQUENCE.
RC TISSUE=Root;
RX MEDLINE=20156257; PubMed=10691991;
RA Choi K.H., Laursen R.A.;
RT "Amino-acid sequence and glycan structures of cysteine proteases with
proline specificity from ginger rhizome Zingiber officinale."
RL Eur. J. Biochem. 267:1516-1526(2000).
CC -!- CATALYTIC ACTIVITY: Preferential cleavage with a proline residue
at P2.
CC -!- SIMILARITY: Belongs to the peptidase C1 family.
DR PIR; A59041; A59041.
DR PDB; 1COD; X-ray; A/B/C/D=1-221.
DR MEROPS; C01.017; -.
DR GlycoSuiteDB; P82474; -.
DR InterPro; IPR000169; Pept_cys_acsite.
DR InterPro; IPR000668; Peptidase_C1.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept_C1; 1.
DR PROSITE; PS00640; THIOI_PROTEASE_ASN; FALSE_NEG.
DR PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; 1.
KW 3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
KW Thiol protease.
FT ACT_SITE 27 27 By similarity.
FT ACT_SITE 161 161 By similarity.
FT DISULFID 24 65 By similarity.
FT DISULFID 58 98 By similarity.
FT DISULFID 155 206 By similarity.
FT CARBOHYD 99 99 N-linked (GlcNAc...)/FTId-CAR_000190.
FT CARBOHYD 156 156 N-linked (GlcNAc...)/FTId-CAR_000200.
FT STRAND 7 8
FT TURN 9 13
FT STRAND 20 20
FT TURN 22 23
FT STRAND 25 25
FT HELIX 27 44
FT STRAND 50 50
FT HELIX 52 58
FT TURN 60 61
FT TURN 64 65
FT STRAND 66 66
FT TURN 70 80
FT TURN 81 81

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FT STRAND 83 83
FT STRAND 85 85
FT TURN 86 88
FT STRAND 107 107
FT STRAND 111 114
FT STRAND 120 127
FT HELIX 128 129
FT STRAND 132 136
FT HELIX 141 144
FT TURN 145 145
FT STRAND 150 151
FT STRAND 161 171
FT TURN 172 173
FT STRAND 174 180
FT STRAND 183 183
FT TURN 185 186
FT TURN 188 188
FT STRAND 189 189
FT TURN 190 191
FT STRAND 192 196
FT TURN 202 203
FT HELIX 205 207
FT TURN 208 209
FT STRAND 213 216
SQ SEQUENCE 221 AA; 23922 MW; 909A312BD8632D42 CRC64;

Query Match 25.8%; Score 311; DB 1; Length 221;
Best Local Similarity 33.8%; Pred. No. 8.8e-20;
Matches 69; Conservative 34; Mismatches 89; Indels 12; Gaps 5;

QY 11 PAEIDLQMTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQLDLAQLVDC-ASQH 69
Db 4 PDSIDWRENGAVPVKNQGGCGSCWAFSTVAAVEGINQIVTGDLISLSEQQLVDCITTAH 63

QY 70 GCHGDTTPRGTEYIOHN-GVVOESYRYRYVAREQSCRRP-NAQRFGISNYCOIYPPNANKI 127
Db 64 GCRGWNPAFOFIVNNGGINSSETYPYRGDGLCNSTVNAVPVVSIDSYENFVSHNQSL 123

QY 128 REALAOTSAIAVIGIKLDAPRH--YDGRITIQRDNGQPNYHVNIVGYSNAQGVY 185
Db 124 QKAVANQVSVTMDAAGRDQLYRSGLFTGSCNISAN-----HALTVVGYGTENDKDF 176

QY 186 WIVRNSWDTWNGDNGYGFANID 209
Db 177 WIVKNSWGNKNGESGYTAEARNIE 200

RESULT 10
CATL_CHICK STANDARD; PRT; 218 AA.
AC P09648;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cathepsin L (EC 3.4.22.15) (Fragments).
GN Name=CTSL;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archaeosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=87304227; PubMed=3305012;
RA Wada K., Takai T., Tanabe T.;
RT "Amino acid sequence of chicken liver cathepsin L.";
RL Eur. J. Biochem. 167:13-18(1987).
RN [2]
RP SEQUENCE OF 1-37 AND 177-216.
RX MEDLINE=87080783; PubMed=3792553; DOI=10.1016/0014-5793(86)81137-1;
RA Wada K., Tanabe T.;
RT "N-terminal amino acid sequences of the heavy and light chains of

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RT chicken liver cathepsin L.";
RL FEBS Lett. 209:330-334(1986).
RN [3]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=88050863; PubMed=3676277;
RA Dufour E., Obled A., Vallin C., Bechet D., Ribadeau-Dumas B.,
RA Huet J.-C.;
RT "Purification and amino acid sequence of chicken liver cathepsin L.";
RL Biochemistry 26:5689-5695(1987).
CC -I- FUNCTION: Important for the overall degradation of proteins in
CC lysosomes.
CC -I- CATALYTIC ACTIVITY: Specificity close to that of papain. As
CC compared to cathepsin B, cathepsin L exhibits higher activity
CC towards protein substrates, but has little activity on Z-Arg-Arg-
CC NHMeC, and no peptidyl-diesterase activity.
CC -I- SUBUNIT: Dimer of a heavy and a light chain linked by disulfide
CC bonds.
CC -I- SUBCELLULAR LOCATION: Lysosomal.
CC -I- SIMILARITY: Belongs to the peptidase C1 family.
DR HSP; P07711; ICLJ.
DR MEROPS; C01.032; -.
DR InterPro; IPR000169; Pept_cys_acsite.
DR InterPro; IPR000668; Peptidase_C1.
DR PRINTS; PR00705; PAPAIN.
DR PRODOM; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept_C1; 1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
KW Direct protein sequencing; Glycoprotein; Hydrolase; Lysosome;
KW Thiol protease.
FT CHAIN 1 176 Cathepsin L heavy chain.
FT NON CONS 176 177
FT CHAIN 177 218 Cathepsin L light chain.
FT ACT_SITE 25 25 By similarity.
FT ACT_SITE 165 165 By similarity.
FT ACT_SITE 185 185 By similarity.
FT CARBOHYD 109 109 N-linked (GlcNAc...).
FT DISULFID 22 65 By similarity.
FT DISULFID 56 99 By similarity.
FT DISULFID 158 207 Interchain (By similarity).
FT CONFLICT 21 21 Q -> I (in Ref. 3).
FT CONFLICT 29 29 S -> N (in Ref. 3).
FT CONFLICT 40 42 RTK -> FKT (in Ref. 3).
FT CONFLICT 97 98 Missing (in Ref. 3).
FT CONFLICT 109 109 N -> K (in Ref. 3).
FT CONFLICT 177 177 Missing (in Ref. 3).
FT CONFLICT 197 197 I -> Q (in Ref. 3).
SQ SEQUENCE 218 AA; 23963 MW; D26B21BC071686C2 CRC64;

Query Match 24.9%; Score 300; DB 1; Length 218;
Best Local Similarity 31.7%; Pred. No. 8.4e-19;
Matches 70; Conservative 37; Mismatches 100; Indels 14; Gaps 7;

QY 10 APAEIDLQMTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQLDLAQLVDC- 66
Db 1 APRSDWREKGYVTPVKDQGGCGSCWAFSTTGALEGHFRTKGLVSLSEQLVDCSRPE 60

QY 67 SQHCHGDTTPRGTEYIOHN-GVVOESYRYRYVAREQSCRRP-NAQRFGISNYCOIYPPN 123
Db 61 GNQCGGLMDQAFQVYVDNGGIDSESYPTAKDDDCRYKAEYNAANDTFVDIPOGH 120

QY 124 ANKIREALAOQTHS-ALAVIIGIKLDAPRH--YDGRITIQRDNGQPNYHVNIVGYSNAQ 182
Db 121 ERALMKAVASVGPVSVDAIDAG---HSSFQYQSGIYEPDCSSEDLDHGVLVVGYGEGG 177

QY 183 VDYWIVRNSWDTWNGDNGYGFAA-----NIDLMMIEEYPVY 219
Db 178 KTYWIVKNSWGNKNGESGYTAEARNIE 218

RESULT 11

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MD01_PSEMR ID MD01_PSEMR STANDARD; PRT; 213 AA.

AC P83443; 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 23-OCT-2004 (Rel. 45, Last annotation update)

DE Macrodontain I (EC 3.4.22.-).

OS Pseudananas macrodotes (Pseudananas sagenarius).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Bromeliaceae;

OC Pseudananas

OX NCBI_TaxID=203992;

RN [1]

RP SEQUENCE, AND TISSUE SPECIFICITY.

RC TISSUE= Fruit;

RA Natalucci C.L., Lopez L.M.I., Brullo A., Maras B., Turk B., Caffini N.O.;

RT "Complete sequence and kinetic aspects of macrodontain I, a cysteine endopeptidase of Pseudananas macrodotes.";

RL Submitted (AUG-2002) to Swiss-Prot.

[2]

RN SEQUENCE OF 1-27, CATALYTIC ACTIVITY, ENZYME REGULATION, SUBUNIT, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.

RC TISSUE= Fruit;

RX MEDLINE=2015315; PubMed=10686143; DOI=10.1006/prsp.1999.1165;

RA Lopez L.M.I., Sequeiros C., Natalucci C.L., Brullo A., Maras B., Barra D., Caffini N.O.;

RT "Purification and characterization of macrodontain I, a cysteine endopeptidase from unripe fruits of Pseudananas macrodotes (Morr.) Harms (Bromeliaceae).";

RL Protein Expr. Purif. 18:133-140 (2000).

CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Ala-[Xaa > Gln]-Xaa > Tyr-Xaa > Leu-[Xaa > Gly]-Xaa.

CC -1- ENZYME REGULATION: Inhibited by E-64 (L-trans-epoxysuccinyl-leucylamide-(4-guanido)-butane).

CC -1- SUBUNIT: Monomer.

CC -1- TISSUE SPECIFICITY: Fruits.

CC -1- MASS SPECTROMETRY: MW=23458.63; METHOD=MALDI; RANGE=1-213; NOTE=Ref.2.

CC -1- MISCELLANEOUS: The optimum pH is 6.1-8.5.

CC -1- SIMILARITY: Belongs to the peptidase C1 family.

DR HSSP; P14080; 1YAL.

DR MEROPS; C01.028; -.

DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IDA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IDA.

DR InterPro; IPR00169; Pept_cys_acsite.

DR InterPro; IPR00668; Peptidase_C1.

DR Pfam; PF00112; Peptidase_C1; 1.

DR PRINTS; PR00705; PAPAIN.

DR ProDom; PD000158; Peptidase_C1; 1.

DR SMART; SM00645; Pept_C1; 1.

DR PROSITE; PS00640; THIOI_PROTEASE ASN; 1.

DR PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.

DR PROSITE; PS00639; THIOI_PROTEASE_HIS; 1.

KW Direct protein sequencing; Hydrolase; Thiol protease.

FT ACT_SITE 26 26 By similarity.

FT ACT_SITE 159 159 By similarity.

FT ACT_SITE 176 176 By similarity.

FT DISULFID 23 63 By similarity.

FT DISULFID 57 96 By similarity.

FT DISULFID 153 201 By similarity.

SQ SEQUENCE 213 AA; 23486 MW; DEB76E632EA77026 CRC64;

Query Match 24.5%; Score 295; DB 1; Length 213;

Best Local Similarity 35.1%; Pred. No. 2.3e-18;

Matches 68; Conservative 30; Mismatches 84; Indels 12; Gaps 7;

QY 11 PAEIDLQRMRTVTPIRMQGGCGSWAFSGVAATESAYLAHRNQSLDLAEQELVDCASOHG 70

DB 3 PQSIDNRDYGAVNEVKNQPGCGGWAFPAIAATVEGIYKIRGNLVYLSEQVELDCAVSYG 62

QY 71 CHGDTIPRGIEY-IOHNGVQESYYRYVAREQSCRRPNAQRFGISNYC--QIYPPNANKI 127

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:32:37 ; Search time 161 Seconds
(without alignments)
533.297 Million cell updates/sec

Title: US-09-867-159A-2

Perfect score: 1206

Sequence: 1 TNACISNGNAPAEIDLQRM.....YFAANIDLMIEEYPYVIL 222

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1481396

Minimum DB seq length: 0

Maximum DB seq length: 222

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1206	100.0	222	5	Aao20568 Cysteine
2	1206	100.0	222	5	Abb98533 Cysteine
3	1203	99.8	222	4	Aau07748 House dus
4	1200	99.5	222	4	Aab98347 D. pteron
5	1196	99.2	222	4	Aau07746 House dus
6	1196	99.2	222	5	Abg67023 House dus
7	1196	99.2	222	8	Adk52140 Der pl al
8	1196	99.2	222	8	Adr87225 Dust mite
9	1189	98.6	222	4	Aau07747 House dus
10	1177	97.6	222	2	Aar52742 Protein a
11	1162	96.4	222	5	Abg67024 House dus
12	1162	96.4	222	5	Abg67030 House dus
13	1161	96.3	222	5	Abg67027 House dus
14	1161	96.3	222	5	Abg67029 House dus
15	1160	96.2	222	5	Abg67036 House dus
16	1159	96.1	222	5	Abg67028 House dus
17	1157	95.9	222	5	Abg67025 House dus
18	1143	94.8	222	5	Abg67032 House dus
19	1142	94.7	222	5	Abg67031 House dus
20	1139	94.4	211	2	Aay25678 Euroglyph
21	1139	94.4	211	7	Adc34926 Euroglyph
22	1133	93.9	222	5	Abg67034 House dus
23	1132	93.9	222	5	Abg67033 House dus
24	982.5	81.5	211	2	Aay25677 Euroglyph
25	982.5	81.5	211	2	Aay25676 Euroglyph

26	982.5	81.5	211	7	ADC34925	Adc34925 Euroglyph
27	982.5	81.5	211	7	ADC34924	Adc34924 Euroglyph
28	949.5	78.7	212	2	AAY25679	Aay25679 Euroglyph
29	949.5	78.7	212	7	ADC34927	Adc34927 Euroglyph
30	472	39.1	86	8	ADR87224	Adr87224 Dust mite
31	472	39.1	159	8	ADR87234	Adr87234 Chimeric
32	460	38.1	86	8	ADR87223	Adr87223 Dust mite
33	430	35.7	81	8	ADR87222	Adr87222 Dust mite
34	430	35.7	153	8	ADR87233	Adr87233 Chimeric
35	407	33.7	72	4	AAU07749	Aau07749 House dus
36	372.5	30.9	181	2	AAW72342	Aaw72342 Dermatoph
37	372.5	30.9	181	2	AAV50544	Aav50544 Dermatoph
38	372.5	30.9	181	4	AAU19147	Aau19147 Synthetic
39	354.5	29.4	181	2	AAW72343	Aaw72343 Dermatoph
40	354.5	29.4	181	2	AAV50545	Aav50545 Dermatoph
41	354.5	29.4	181	4	AAU19148	Aau19148 Synthetic
42	308.5	25.6	211	2	AAW44779	Aaw44779 Human cat
43	303	25.1	217	8	ADL92138	Adl92138 Chymopapa
44	301.5	25.0	190	3	AAV83106	Aav83106 DI4059 pr
45	295	24.5	215	5	AAE28367	Aae28367 Dirofilar

ALIGNMENTS

RESULT 1
AAO20568
ID AAO20568 standard; protein; 222 AA.
XX
AC AAO20568;
XX
DT 02-JAN-2003 (first entry)
XX
DE Cysteine protease protein.
XX
KW Antiallergic; antiinflammatory; antiasthmatic; dermatological; allergen;
KW anti-histamine; histamine synthesis inhibitor; allergic hypersensitivity;
KW allergic asthma; allergic rhinitis; cysteine protease protein; enzyme;
KW atopic eczema.
XX
OS Dermatophagoides pteronyssinus.
XX
FH Key Location/Qualifiers
FT Misc-difference 105 /note= "Encoded by ACC"
XX
PN WO200278736-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-FR001098.
XX
PR 30-MAR-2001; 2001FR-00004370.
PR 03-MAY-2001; 2001FR-00005929.
PR 29-MAY-2001; 2001US-00867159.
XX
(ANTI-) ANTIALIS SARR.
XX
PI Loria E, Terrasse G, Trehin Y;
XX
DR WPI; 2002-750636/81.
DR N-PSDB; AAL41281.
XX
XX
PT Antiallergic compositions containing an anti-histamine, a histamine
PT synthesis inhibitor, and optionally an allergen or nucleic acid coding
PT for the allergen.
XX
PS Claim 13; Page 30-31; 32pp; French.
XX
CC The invention relates to antiallergic compositions containing an anti-
CC histamine, a histamine synthesis inhibitor, and optionally an allergen or
CC isolated nucleic acid molecule that has at least one polynucleotide
CC sequence coding for the allergen, together with a pharmaceutical carrier.

CC The pharmaceutical composition of the invention is useful as a non-
 CC specific anti-allergic treatment, and also useful in the treatment of
 CC allergic hypersensitivity, allergic asthma, allergic rhinitis, and
 CC allergic and atopic eczema. This sequence represents the cysteine
 CC proenzyme protein relating to the anti-allergic compositions of the
 CC invention
 XX
 XX Sequence 222 AA;

Query Match 100.0%; Score 1206; DB 5; Length 222;
 Best Local Similarity 100.0%; Pred. No. 2.7e-127;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNACISNGNAPAEIDLRQMTVTPIRMGGCGGSCWAFSGVAATESAYLAHRNQSJDLAEQ 60
 DB 1 TNACISNGNAPAEIDLRQMTVTPIRMGGCGGSCWAFSGVAATESAYLAHRNQSJDLAEQ 60
 QY 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVVQESYRYVAREQSCRPNQRFGISNYCQIY 120
 DB 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVVQESYRYVAREQSCRPNQRFGISNYCQIY 120
 QY 121 PNANKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
 DB 121 PNANKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
 QY 181 QGVYWIIVRNSWDTNWGNGYGYFAANIDLMWIEEYPYVWIL 222
 DB 181 QGVYWIIVRNSWDTNWGNGYGYFAANIDLMWIEEYPYVWIL 222

RESULT 2

ABB98533
 ID ABB98533 standard; protein; 222 AA.

XX ABB98533;
 AC ABB98533;

DT 13-DEC-2002 (first entry)

DE Cysteine protease.

XX Antiallergic; antiasthmatic; antiinflammatory; dermatological;
 KW immunotherapy; allergen; allergic hypersensitivity reaction;
 KW allergic asthma; allergic rhinitis; allergic atopic eczema;
 KW cysteine protease.

OS Dermatophagoides pteronyssinus.

XX
 FH Key Location/Qualifiers
 FT Misc-difference 105
 FT /note= "Encoded by CCA"

PN FR2822709-A1.

PD 04-OCT-2002.

PF 03-MAY-2001; 2001FR-00005929.

PR 30-MAR-2001; 2001FR-00004370.

XX (ANTI-) ANTIALIS SARL.

PI Loria E, Terrasse G, Trehin Y;

XX WPI; 2002-735037/80.

DR N-PSDB; ABQ80833.

XX Antiallergic composition, useful for preventing and treating e.g. asthma,
 PT rhinitis or eczema, containing at least two of allergen, antihistamine
 PT and histamine synthesis inhibitor.

PS Claim 7; Page 27-28; 33pp; French.

XX The present invention relates to an anti-allergic pharmaceutical

CC composition (I) comprising a pharmaceutical carrier containing an active
 CC agent combination of at least two of: an allergen; an antihistamine; and
 CC a histamine synthesis inhibitor. (I) is used for treating or preventing
 CC allergic hypersensitivity reactions, especially allergic asthma, allergic
 CC rhinitis or allergic atopic eczema, in babies, children or adults. The
 CC present sequence is cysteine protease from Dermatophagoides
 CC pteronyssinus, which was used as an allergen in the invention
 XX
 XX Sequence 222 AA;

Query Match 100.0%; Score 1206; DB 5; Length 222;
 Best Local Similarity 100.0%; Pred. No. 2.7e-127;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNACISNGNAPAEIDLRQMTVTPIRMGGCGGSCWAFSGVAATESAYLAHRNQSJDLAEQ 60
 DB 1 TNACISNGNAPAEIDLRQMTVTPIRMGGCGGSCWAFSGVAATESAYLAHRNQSJDLAEQ 60
 QY 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVVQESYRYVAREQSCRPNQRFGISNYCQIY 120
 DB 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVVQESYRYVAREQSCRPNQRFGISNYCQIY 120
 QY 121 PNANKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
 DB 121 PNANKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
 QY 181 QGVYWIIVRNSWDTNWGNGYGYFAANIDLMWIEEYPYVWIL 222
 DB 181 QGVYWIIVRNSWDTNWGNGYGYFAANIDLMWIEEYPYVWIL 222

RESULT 3

AAU07748
 ID AAU07748 standard; protein; 222 AA.

XX AAU07748;

DT 04-DEC-2001 (first entry)

DE House dust mite allergenic protein Der p I variant d.

XX House dust mite; allergenic protein; Der p I; Der p II; Der f I;
 KW Der f II; antiallergenic; immunostimulant; house dust mite allergy;
 KW T-cell epitope; polymorphic variant.

OS Dermatophagoides pteronyssinus.

XX
 FH Key Location/Qualifiers
 FT Misc-difference 136
 FT /note= "Wild-type Ser substituted by Thr"

PN US6268491-B1.

PD 31-JUL-2001.

PF 07-JUN-1995; 95US-00484296.

PR 16-OCT-1991; 91US-00777859.

PR 08-MAY-1992; 92US-00881396.

PR 14-APR-1993; 93WO-US003471.

PR 14-APR-1994; 94US-00227772.

PR 19-MAY-1995; 95US-00445307.

XX (IMMU-) IMMULOGIC PHARM CORP.

PA Garman RD, Greenstein JL, Kuo M, Rogers BL, Franzen HM, Chen X;

PI Evans S, Shaked Z;

XX WPI; 2001-549074/61.

XX Peptides comprising T cell groups of the major allergens from
 PT Dermatophagoides (house dust mites), useful for treating house dust mite
 PT allergy in humans, and for diagnosing sensitivity to house dust mite

PT protein allergens.
 XX Disclosure; Fig 22; 158pp; English.
 XX The invention relates to an isolated peptide of the major protein
 CC allergens of the genus Dermatophagoides, which comprises at least one T
 CC cell group of a protein allergen from Der p (DP) I, DP II, Der f (DF) I
 CC or DF II. The isolated peptide comprises at least two regions, each
 CC region comprising at least one T cell group of a protein allergen of the
 CC genus Dermatophagoides. The regions are derived from the same or
 CC different protein allergens of the genus Dermatophagoides. The peptides
 CC are useful for treating house dust mite allergy in humans. The peptides
 CC are also useful for detecting or diagnosing sensitivity to house dust
 CC mite protein allergens. The present peptides have similar or enhanced
 CC therapeutic properties as the naturally-occurring allergen, but have
 CC reduced side effects, and increased solubility and stability. The present
 CC sequence represents an allergenic protein from Dermatophagoides from
 CC which the T-cell epitope containing peptides are derived, a polymorphic
 CC variant of Der p I. Note: The present sequence is not shown in the
 CC specification but is derived from the Der p I sequence shown in figure 22
 XX
 SQ Sequence 222 AA;
 Query Match 99.8%; Score 1203; DB 4; Length 222;
 Best Local Similarity 99.5%; Pred. No. 5.8e-127;
 Matches 221; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNACISNGNAPAEIDLQMRVTVPTRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 60
 DB 1 TNACISNGNAPAEIDLQMRVTVPTRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 60
 QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQVQSYRYVAREQSCRRPNAQRFGISNYCOIY 120
 DB 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQVQSYRYVAREQSCRRPNAQRFGISNYCOIY 120
 QY 121 PPNAKIREALAOHTSAIAVIGIKDLDAFRHYDGRITIIQRDNGVQPNYHAVNIVGYNSA 180
 DB 121 PPNAKIREALAOHTSAIAVIGIKDLDAFRHYDGRITIIQRDNGVQPNYHAVNIVGYNSA 180
 QY 181 QGVVDYWIVRNSWDNTNWDNGVGYFAANIDLMWIEEYPVWIL 222
 DB 181 QGVVDYWIVRNSWDNTNWDNGVGYFAANIDLMWIEEYPVWIL 222
 RESULT 4
 AAB98347
 ID AAB98347 standard; protein; 222 AA.
 XX AAB98347;
 XX 21-AUG-2001 (first entry)
 XX D. pteronyssinus Der p 1 protein SEQ ID NO:82.
 DE Mite group 1 protein; methyltrophic yeast; Escherichia coli; allergy;
 KW recombinant mite group 1 protein; allergic response; antiallergic;
 KW infectious disease; allergic disease.
 XX Dermatophagoides pteronyssinus.
 XX WO200129078-A2.
 XX 26-APR-2001.
 XX 12-OCT-2000; 2000WO-US028204.
 XX 15-OCT-1999; 99US-0159841P.
 XX (HESK-) HESKA CORP.
 XX Best EA, Modermott MJ;
 XX WPI; 2001-308475/32.
 DR

DR N-PSDB; AAB22385.
 XX Producing recombinant mite Group 1 protein for treating allergies,
 PT involves culturing a methyltrophic yeast microorganism or Escherichia
 PT coli transformed with nucleic acid molecule, and recovering the protein.
 XX Claim 12; Page 145; 154pp; English.
 XX The present invention describes a method for the production of a
 CC recombinant mite Group 1 protein (I). The method comprises culturing a
 CC methyltrophic yeast microorganism transformed with a nucleic acid
 CC molecule (II) encoding (I), and recovering (I), or culturing Escherichia
 CC coli transformed with (II), under conditions in which (I) forms an
 CC inclusion body in E. coli, isolating the inclusion body, and recovering
 CC (I). Also described is a method for detecting mite allergy in an animal
 CC comprising: (a) contacting (I) with a putative IGE-containing substance
 CC to form a complex between (I) and IGE; and (b) determining the presence of
 CC of IGE reactive with (I) by detecting the complex, where the presence of
 CC reactive IGE is indicative of mite allergy in the animal. (I) is useful
 CC for detecting mite allergy in an animal, or in a composition to reduce
 CC allergic response to a mite Group 1 protein in a mite allergic animal.
 CC (I) is also useful in a composition for treating or preventing allergic,
 CC infectious or other diseases. AAB22326 to AAB22394 and AAB98326 to
 CC AAB98349 represent sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 222 AA;
 Query Match 99.5%; Score 1200; DB 4; Length 222;
 Best Local Similarity 99.5%; Pred. No. 1.3e-126;
 Matches 221; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNACISNGNAPAEIDLQMRVTVPTRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 60
 DB 1 TNACISNGNAPAEIDLQMRVTVPTRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 60
 QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQVQSYRYVAREQSCRRPNAQRFGISNYCOIY 120
 DB 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQVQSYRYVAREQSCRRPNAQRFGISNYCOIY 120
 QY 121 PPNAKIREALAOHTSAIAVIGIKDLDAFRHYDGRITIIQRDNGVQPNYHAVNIVGYNSA 180
 DB 121 PPNAKIREALAOHTSAIAVIGIKDLDAFRHYDGRITIIQRDNGVQPNYHAVNIVGYNSA 180
 QY 181 QGVVDYWIVRNSWDNTNWDNGVGYFAANIDLMWIEEYPVWIL 222
 DB 181 QGVVDYWIVRNSWDNTNWDNGVGYFAANIDLMWIEEYPVWIL 222
 RESULT 5
 AAU07746
 ID AAU07746 standard; protein; 222 AA.
 XX AAU07746;
 XX 04-DEC-2001 (first entry)
 XX House dust mite allergenic protein Der p I variant b.
 DE House dust mite; allergenic protein; Der p I; Der p II; Der f I;
 KW Der f II; antiallergic; immunostimulant; house dust mite allergy;
 KW T-cell epitope; polymorphic variant.
 XX Dermatophagoides pteronyssinus.
 XX Key Location/Qualifiers
 FT Misc-difference 50 /note= "Wild-type His substituted by Tyr"
 FT Misc-difference 124 /note= "Wild-type Ala substituted by Val"
 FT US6268491-B1.
 XX

PD 31-JUL-2001.
XX
XX 07-JUN-1995; 95US-00484296.
XX
PR 16-OCT-1991; 91US-00777859.
PR 08-MAY-1992; 92US-00881396.
PR 14-APR-1993; 93WO-US003471.
PR 14-APR-1994; 94US-00227772.
PR 19-MAY-1995; 95US-00445307.
XX
XX (IMMU-) IMMUNOLOGIC PHARM CORP.
PA
XX Garman RD, Greenstein JL, Kuo M, Rogers BL, Franzen HM, Chen X;
PI Evans S, Shaked Z;
XX WPI; 2001-549074/61.
XX
XX Peptides comprising T cell groups of the major allergens from
PT Dermatophagoides (house dust mites), useful for treating house dust mite
PT allergy in humans, and for diagnosing sensitivity to house dust mite
PT protein allergens.
XX
XX Disclosure; Fig 22; 158pp; English.
XX
XX The invention relates to an isolated peptide of the major protein
CC allergens of the genus Dermatophagoides, which comprises at least one T
CC cell group of a protein allergen from Der p (DP) I, DP II, Der f (DF) I
CC or DF II. The isolated peptide comprises at least two regions, each
CC region comprising at least one T cell group of a protein allergen of the
CC genus Dermatophagoides. The regions are derived from the same or
CC different protein allergens of the genus Dermatophagoides. The peptides
CC are useful for treating house dust mite allergy in humans. The peptides
CC are also useful for detecting or diagnosing sensitivity to house dust
CC mite protein allergens. The present peptides have similar or enhanced
CC therapeutic properties as the naturally-occurring allergen, but have
CC reduced side effects, and increased solubility and stability. The present
CC sequence represents an allergenic protein from Dermatophagoides from
CC which the T-cell epitope containing peptides are derived, a polymorphic
CC variant of Der p I. Note: The present sequence is not shown in the
CC specification but is derived from the Der p I sequence shown in figure 22
XX
XX Sequence 222 AA;
XX
Query Match 99.2%; Score 1196; DB 4; Length 222;
Best Local Similarity 99.1%; Pred. No. 3.6e-126;
Matches 220; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 TNACSGNAPAEIDLQMTVTPIRMQGGCGSWAFSGVAATESAYLAHRNOSLDLAEQ 60
DB 1 TNACSGNAPAEIDLQMTVTPIRMQGGCGSWAFSGVAATESAYLAHRNOSLDLAEQ 60
QY 61 ELVDCAHQCHGDTIPRGIEYIQHGVVQESYRVVAREQSCRRPNAQRFGLSNVCQIY 120
DB 61 ELVDCAHQCHGDTIPRGIEYIQHGVVQESYRVVAREQSCRRPNAQRFGLSNVCQIY 120
QY 121 PPNANKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIGYSNA 180
DB 121 PPNVKNIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIGYSNA 180
QY 181 QGVDDYIVRNSWDTNWDNGNGYGFYFAANIDLMIEEYPPVVIL 222
DB 181 QGVDDYIVRNSWDTNWDNGNGYGFYFAANIDLMIEEYPPVVIL 222
RESULT 6
ABG67023
ID ABG67023 standard; protein; 222 AA.
XX
XX AC ABG67023;
XX
XX AC ABG67023;
DT 24-SEP-2002 (first entry)
XX
XX DE House dust mite allergen Der p 1.
XX
XX Immunoglobulin E; IGE; allergen; allergy; hay fever; rhinoconjunctivitis;
KW rhinitis; asthma; systemic anaphylaxis; vaccine; antiallergic;
KW B cell epitope.
XX
XX Dermatophagoides pteronyssinus.
OS
XX WO200240676-A2.
PN
XX 23-MAY-2002.
PD
XX 16-NOV-2001; 2001WO-DK000764.
XX
XX 16-NOV-2000; 2000DK-00001718.
PR
XX 16-NOV-2000; 2000US-0249361P.
PR
XX 14-JUN-2001; 2001US-0298170P.
XX
XX (ALKA-) ALK-ABELLO AS.
PA
XX Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
PI
XX WPI; 2002-508328/54.
DR
XX N-PSDB; ABK95639.
XX
XX New recombinant mutant allergen, useful for preventing and/or treating
PT allergy, comprises multiple mutations and reduced immunoglobulin E
PT binding affinity.
XX
XX Example 7; Page 103-104; 210pp; English.
XX
XX The invention relates to a recombinant allergen (I) which is a mutant of
CC a naturally occurring allergen, where the mutant allergen has at least
CC four primary mutations, which each reduce the specific immunoglobulin E
CC (IGE) binding capability of the mutated allergen as compared to the IGE
CC binding capability of the naturally occurring allergen, where each
CC primary mutation is a substitution of one surface-exposed amino acid
CC residue with another residue, which does not occur in the same position
CC in the amino acid sequence of any known homologous protein within the
CC taxonomic species from which the naturally occurring allergen originates,
CC and each primary mutation is spaced from each other primary mutation by
CC at least 15 Angstrom, and the primary mutations are placed in such a
CC manner that at least one circular surface region with a area of 800
CC Angstrom² comprises no mutation. Also included are a composition
CC comprising two or more of the recombinant allergens, where the variant
CC allergen is defined by having at least one primary mutation, which is
CC absent in at least one of the other variants, and for each variant no
CC secondary mutation is present within a radius of 15 Angstrom from each
CC absent primary mutation; a DNA sequence encoding the recombinant allergen
CC or its derivative, partial sequence or degenerated sequence, or a
CC sequence which hybridises to it under stringent conditions, where the
CC derivative, partial sequence, degenerated sequence or hybridising
CC sequence encodes a peptide having at least one B cell epitope; an
CC expression vector comprising the DNA and a host cell comprising the
CC vector. The recombinant allergen is useful as a pharmaceutical, for
CC preparing a pharmaceutical for preventing and/or treating allergy, or in
CC a diagnostic assay for assessing relevance, safety or outcome of therapy
CC of a subject, where an IGE containing sample of the subject is mixed with
CC the recombinant allergen and assessed for the level of reactivity between
CC the IGE in the sample and the recombinant allergen. The recombinant
CC allergen or compositions are useful for generating an immune response in
CC a subject, for vaccination or treatment of a subject or for the
CC treatment, prevention or alleviation of allergic reactions in a subject
CC e.g. hay fever, rhinoconjunctivitis, rhinitis, asthma or systemic
CC anaphylaxis. The present sequence represents a wild-type allergen of the
CC invention
XX
XX Query Match 99.2%; Score 1196; DB 5; Length 222;
Best Local Similarity 99.1%; Pred. No. 3.6e-126;
Matches 220; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 TNACSGNAPAEIDLQMTVTPIRMQGGCGSWAFSGVAATESAYLAHRNOSLDLAEQ 60

Db 1 TNACSSINGNAPAEIDLROMETVTPIRMGGCGSWAFSGVAATESAYLAHRNOSLDLAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
Db 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
QY 121 PPNANKIREALAOQTHSAIAIIGIKOLDAPFRHYDGRITIIQORDNGYQPNYHVNIVGYSNA 180
Db 121 PPNANKIREALAOQTHSAIAIIGIKOLDAPFRHYDGRITIIQORDNGYQPNYHVNIVGYSNA 180
QY 181 QGVYDIWVRNSWDTNWDNGYGYFAANIDLMLMIEEYPYVVIL 222
Db 181 QGVYDIWVRNSWDTNWDNGYGYFAANIDLMLMIEEYPYVVIL 222

RESULT 7
ADK52140
ID ADK52140 standard; protein; 222 AA.
XX AC ADK52140;
XX DT 06-MAY-2004 (first entry)
XX DE Der p1 allergen.
XX KW recombinant protein allergen; Antiallergic; Desensitization; antibody;
XX KW allergy; house dust mite; allergen.
XX OS Dermatophagoides pteronyssinus.
XX PN WO2004005334-A2.
XX PD 15-JAN-2004.
XX PF 04-JUL-2003; 2003WO-FR002085.
XX PR 05-JUL-2002; 2002FR-00008485.
XX PA (STAL-) STALLERGENES SA.
XX PA (SETB) SOC NAT EXPL IND TABACS & ALLUMETTES.
XX PI Gomord V, Lienard D, Van Ree R, Van Oort E, Dorlhac De Borne F;
PI Didier Laurent A, Faye L;
XX WPI: 2004-083498/08.
XX DR N-PSDB; ADK52139.
XX PT Recombinant production of acarid protein allergen, useful for diagnosis
XX PT and treatment of allergy to house dust mites, comprises growing
XX PT transformed eukaryotes, particularly plants.
XX PS Claim 4; SEQ ID NO 2; 55pp; French.
XX CC The present invention relates to a method for production of a recombinant
XX CC protein allergen from an acarid of the genera Dermatophagoides or
XX CC Euroglyphus. The allergens and also antibodies raised against them, are
XX CC useful for diagnosis and treatment of allergies to house dust mites. When
XX CC expressed in plants, allergens are synthesized and matured to
XX CC biologically active form, with essentially the same pattern of
XX CC glycosylation as the native protein. Recombinant expression provides a
XX CC pure protein; contrast complex mixtures of allergens currently used. The
XX CC present sequence represents Der p1 allergen.
XX SQ Sequence 222 AA;

Query Match 99.2%; Score 1196; DB 8; Length 222;
Best Local Similarity 99.1%; Pred. No. 3.6e-126;
Matches 220; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 TNACSSINGNAPAEIDLROMETVTPIRMGGCGSWAFSGVAATESAYLAHRNOSLDLAEQ 60
Db 1 TNACSSINGNAPAEIDLROMETVTPIRMGGCGSWAFSGVAATESAYLAHRNOSLDLAEQ 60

QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
Db 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
QY 121 PPNANKIREALAOQTHSAIAIIGIKOLDAPFRHYDGRITIIQORDNGYQPNYHVNIVGYSNA 180
Db 121 PPNANKIREALAOQTHSAIAIIGIKOLDAPFRHYDGRITIIQORDNGYQPNYHVNIVGYSNA 180
QY 181 QGVYDIWVRNSWDTNWDNGYGYFAANIDLMLMIEEYPYVVIL 222
Db 181 QGVYDIWVRNSWDTNWDNGYGYFAANIDLMLMIEEYPYVVIL 222

RESULT 8
ADR87225
ID ADR87225 standard; protein; 222 AA.
XX AC ADR87225;
XX DT 16-DEC-2004 (first entry)
XX DE Dust mite allergen Der p 1 SEQ ID NO:14.
XX KW dust mite; allergen; Der p 1; T-cell response; IgE; immunoglobulin E;
XX KW immune response; antiallergic; gene therapy; vaccine.
XX OS Dermatophagoides sp.
XX PN WO2004081028-A2.
XX PD 23-SEP-2004.
XX PF 15-MAR-2004; 2004WO-IB001300.
XX PR 14-MAR-2003; 2003US-0455004P.
XX PR 12-MAR-2004; 2004US-00799514.
XX PA (UYLA-) UNIV LAUSANNE.
XX PI Spertini F;
XX WPI: 2004-668931/65.
XX PT New compositions including contiguous overlapping peptide fragments that
XX PT form an entire amino acid sequence of an allergen (e.g. bee venom or
XX PT birch pollen allergen), useful for preventing or treating IgE-mediated
XX PT allergies.
XX PS Claim 4; SEQ ID NO 14; 82pp; English.
XX CC The invention relates to novel compositions including contiguous
XX CC overlapping peptide fragments which together form an entire amino acid
XX CC sequence of an allergen, where the fragments are capable of inducing a T-
XX CC cell response in patients who are hypersensitive to the allergen. The
XX CC contiguous overlapping peptide fragments further result in lower levels
XX CC of IgE stimulation activity. The lower levels of IgE stimulation activity
XX CC are zero or weak. The contiguous overlapping peptide fragments further
XX CC result in a decrease in T-cell response upon subsequent exposure to the
XX CC allergen, thus, modulating an immune response in the patients, who are
XX CC hypersensitive to the allergen. A composition of the invention has
XX CC antiallergic activity, and may have a use in gene therapy, and as a
XX CC vaccine. The composition and methods are useful for preventing or
XX CC treating IgE-mediated allergies. The present sequence represents an
XX CC allergen of the invention, dust mite Der p 1.
XX SQ Sequence 222 AA;

Query Match 99.2%; Score 1196; DB 8; Length 222;
Best Local Similarity 99.1%; Pred. No. 3.6e-126;
Matches 220; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 TNACSSINGNAPAEIDLROMETVTPIRMGGCGSWAFSGVAATESAYLAHRNOSLDLAEQ 60

Db 1 TNACSGNAPAEIDLQRMRTVTPIRMQGGSCSWAFSGVAATESAYLAHRNQLDLAEQ 60
QY 61 ELVDCASQHGCHGDTTPRGIEYIQHNGVQVESYRYVAREQSCRRPNAORFGISNYCQIY 120
Db 61 ELVDCASQHGCHGDTTPRGIEYIQHNGVQVESYRYVAREQSCRRPNAORFGISNYCQIY 120
QY 121 PPNANKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYOPNHYAVNIVGYSNA 180
Db 121 PPNANKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYOPNHYAVNIVGYSNA 180
QY 181 QGVYWIWRNSWDTNMGDNGYGYFAANIDLMMEIEEYPYVVIL 222
Db 181 QGVYWIWRNSWDTNMGDNGYGYFAANIDLMMEIEEYPYVVIL 222

RESULT 9
AAU07747
ID AAU07747 standard; protein; 222 AA.
AC AAU07747;
XX
XX
DT 04-DEC-2001 (first entry)
DE House dust mite allergenic protein Der p I variant c.
XX
XX House dust mite; allergenic protein; Der p I; Der p II; Der f I;
KW Der f II; anti-allergenic; immunostimulant; house dust mite allergy;
KW T-cell epitope; polymorphic variant.
XX
OS Dermatophagoides pteronyssinus.
XX
XX Key Location/Qualifiers
FT Misc-difference 50 /note= "Wild-type His substituted by Tyr"
FT Misc-difference 81 /note= "Wild-type Glu substituted by Lys"
FT Misc-difference 124 /note= "Wild-type Ala substituted by Val"
FT Misc-difference 215 /note= "Wild-type Glu substituted by Gln"
XX
XX US6268491-B1.
XX
XX 31-JUL-2001.
XX
XX 07-JUN-1995; 95US-00484296.
XX
XX 16-OCT-1991; 91US-00777859.
XX 08-MAY-1992; 92US-00881396.
XX 14-APR-1993; 93WO-US003471.
XX 14-APR-1994; 94US-00227772.
XX 19-MAY-1995; 95US-00445307.
XX
XX (IMMU-) IMMULOGIC PHARM CORP.
XX
XX Garman RD, Greenstein JL, Kuo M, Rogers BL, Franzen HM, Chen X;
PI Evans S, Shaked Z;
XX
XX WPI; 2001-549074/61.
XX
XX Peptides comprising T cell groups of the major allergens from
PT Dermatophagoides (house dust mites), useful for treating house dust mite
PT allergy in humans, and for diagnosing sensitivity to house dust mite
PT protein allergens.
XX
XX Disclosure; Fig 22; 158pp; English.
XX
XX The invention relates to an isolated peptide of the major protein
CC allergens of the genus Dermatophagoides, which comprises at least one T
CC cell group of a protein allergen from Der p (DP) I, DP II, Der f (DF) I
CC or DF II. The isolated peptide comprises at least two regions, each
CC region comprising at least one T cell group of a protein allergen of the

CC genus Dermatophagoides. The regions are derived from the same or
CC different protein allergens of the genus Dermatophagoides. The peptides
CC are useful for treating house dust mite allergy in humans. The peptides
CC are also useful for detecting or diagnosing sensitivity to house dust
CC mite protein allergens. The present peptides have similar or enhanced
CC therapeutic properties as the naturally-occurring allergen, but have
CC reduced side effects, and increased solubility and stability. The present
CC sequence represents an allergenic protein from Dermatophagoides from
CC which the T-cell epitope containing peptides are derived, a polymorphic
CC variant of Der p I. Note: The present sequence is not shown in the
CC specification but is derived from the Der p I sequence shown in figure 22
XX
XX Sequence 222 AA;
QY

Query Match 98.6%; Score 1189; DB 4; Length 222;
Best Local Similarity 98.2%; Pred. No. 2.2e-125;
Matches 218; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 TNACSGNAPAEIDLQRMRTVTPIRMQGGSCSWAFSGVAATESAYLAHRNQLDLAEQ 60
Db 1 TNACSGNAPAEIDLQRMRTVTPIRMQGGSCSWAFSGVAATESAYLAHRNQLDLAEQ 60
QY 61 ELVDCASQHGCHGDTTPRGIEYIQHNGVQVESYRYVAREQSCRRPNAORFGISNYCQIY 120
Db 61 ELVDCASQHGCHGDTTPRGIEYIQHNGVQVESYRYVAREQSCRRPNAORFGISNYCQIY 120
QY 121 PPNANKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYOPNHYAVNIVGYSNA 180
Db 121 PPNANKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYOPNHYAVNIVGYSNA 180
QY 181 QGVYWIWRNSWDTNMGDNGYGYFAANIDLMMEIEEYPYVVIL 222
Db 181 QGVYWIWRNSWDTNMGDNGYGYFAANIDLMMEIEEYPYVVIL 222

RESULT 10
AAR52742
ID AAR52742 standard; protein; 222 AA.
XX
XX AAR52742;
XX
XX 25-MAR-2003 (revised)
DT 17-OCT-1994 (first entry)
XX
XX Protein allergen of Der pI.
XX
XX Der pI; House Dust Mite Allergen.
XX
XX Dermatophagoides pteronyssinus.
XX
XX Key Location/Qualifiers
FT Misc-difference 50 /label= His or Tyr
FT Misc-difference 81 /label= Glu or Lys
FT Misc-difference 124 /label= Ala or Val
FT Misc-difference 136 /label= Ser or Thr
FT Misc-difference 215 /label= Glu or Gln
XX
XX WO9405790-A1.
XX
XX 17-MAR-1994.
XX
XX 10-SEP-1993; 93WO-US008518.
XX
XX 10-SEP-1992; 92US-00945288.
XX
XX (IMMU-) IMMULOGIC PHARM CORP.
XX
XX Thomas WR, Chua K;
PI

XX WPI; 1994-101195/12.
 XX
 PT New protein allergens of house dust mite - used for diagnosing and
 PT treating sensitivity in an individual to house dust mite allergens.
 XX
 PS Disclosure; Fig 18; 98pp; English.
 XX
 CC AAR52742 is a mature Der pI mite allergen. The mature protein can be used
 CC to detect sensitivity in an individual to house dust mite and to reduce
 CC the sensitivity of the individual. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 222 AA;
 Query Match 97.6%; Score 1177; DB 2; Length 222;
 Best Local Similarity 97.7%; Pred. No. 5.1e-124;
 Matches 217; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TNACSSINGNAPAEIDLRQMTVTPIRMQGGCGSWAFSGVAATESAYLAHRNQSLLDAEQ 60
 DB 1 TNACSSINGNAPAEIDLRQMTVTPIRMQGGCGSWAFSGVAATESAYLAHRNQSLLDAEQ 60
 QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVWQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
 DB 61 ELVDCASQHGCHGDTIPRGIXYIQHNGVWQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
 QY 121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 180
 DB 121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 180
 QY 181 QGVYDWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVIL 222
 DB 181 QGVYDWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVIL 222
 RESULT 11
 ABG67024
 ID ABG67024 standard; protein; 222 AA.
 AC
 XX ABG67024;
 AC
 XX 24-SEP-2002 (first entry)
 DT House dust mite allergen Der p 1 mutant #1.
 DE
 XX Immunoglobulin E; IgE; allergen; allergy; mite; hay fever;
 KW rhinoconjunctivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
 KW vaccine; antiallergic; B cell epitope.
 XX
 OS Dermatophagoides pteronyssinus.
 OS Synthetic.
 XX
 PN WO200240676-A2.
 XX
 XX 23-MAY-2002.
 XX
 XX 16-NOV-2001; 2001WO-DK000764.
 XX
 PR 16-NOV-2000; 2000DK-00001718.
 PR 16-NOV-2000; 2000US-0249361P.
 PR 14-JUN-2001; 2001US-0298170P.
 XX
 PA (ALKA-) ALK-ABELLO AS.
 XX
 PI Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
 XX
 XX WPI; 2002-508328/54.
 DR N-PSDB; ABK95640.
 XX
 XX New recombinant mutant allergen, useful for preventing and/or treating
 PT allergy, comprises multiple mutations and reduced immunoglobulin E
 PT binding affinity.

XX
 PS Example 7; Page; 210pp; English.
 XX
 CC The invention relates to a recombinant allergen (I) which is a mutant of
 CC a naturally occurring allergen, where the mutant allergen has at least
 CC four primary mutations, which each reduce the specific immunoglobulin E
 CC (IgE) binding capability of the mutated allergen as compared to the IgE
 CC binding capability of the naturally occurring allergen, where each
 CC primary mutation is a substitution of one surface-exposed amino acid
 CC residue with another residue, which does not occur in the same position
 CC in the amino acid sequence of any known homologous protein within the
 CC taxonomic species from which the naturally occurring allergen originates,
 CC and each primary mutation is spaced from each other primary mutation by
 CC at least 15 Angstrom , and the primary mutations are placed in such a
 CC manner that at least one circular surface region with a area of 800
 CC Angstrom ^2 comprises no mutation. Also included are a composition
 CC comprising two or more of the recombinant allergens, where the variant
 CC allergen is defined by having at least one primary mutation, which is
 CC absent in at least one of the other variants, and for each variant no
 CC secondary mutation is present within a radius of 15 Angstrom from each
 CC absent primary mutation; a DNA sequence encoding the recombinant allergen
 CC or its derivative, partial sequence or degenerated sequence, or a
 CC sequence which hybridises to it under stringent conditions, where the
 CC derivative, partial sequence, degenerated sequence or hybridising
 CC sequence encodes a peptide having at least one B cell epitope; an
 CC expression vector comprising the DNA and a host cell comprising the
 CC vector. The recombinant allergen is useful as a pharmaceutical, for
 CC preparing a pharmaceutical for preventing and/or treating allergy, or in
 CC a diagnostic assay for assessing relevance, safety or outcome of therapy
 CC of a subject, where an IgE containing sample of the subject is mixed with
 CC the recombinant allergen and assessed for the level of reactivity between
 CC the IgE in the sample and the recombinant allergen. The recombinant
 CC allergen or compositions are useful for generating an immune response in
 CC a subject, for vaccination or treatment of a subject or for the
 CC treatment, prevention or alleviation of allergic reactions in a subject
 CC e.g. hay fever, rhinoconjunctivitis, rhinitis, asthma or systemic
 CC anaphylaxis. The present sequence represents a recombinant allergen of
 CC the invention. Note: The present sequence was not shown in the
 CC specification but was created by the indexer using information in the
 CC specification and the corresponding wild-type sequence
 XX
 SQ Sequence 222 AA;
 Query Match 96.4%; Score 1162; DB 5; Length 222;
 Best Local Similarity 96.8%; Pred. No. 2.5e-122;
 Matches 215; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TNACSSINGNAPAEIDLRQMTVTPIRMQGGCGSWAFSGVAATESAYLAHRNQSLLDAEQ 60
 DB 1 TNACSSINGNAPAEIDLRQMTVTPIRMQGGCGSWAFSGVAATESAYLAHRNQSLLDAEQ 60
 QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVWQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
 DB 61 ELVDCASQHGCHGDTIPQIEYIQHNGVWQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
 QY 121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 180
 DB 121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 180
 QY 181 QGVYDWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVIL 222
 DB 181 QGVYDWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVIL 222
 RESULT 12
 ABG67030
 ID ABG67030 standard; protein; 222 AA.
 XX
 XX ABG67030;
 AC
 XX 24-SEP-2002 (first entry)
 DT House dust mite allergen Der p 1 mutant #7.
 XX
 DE

XX Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever;
 KW rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
 KW vaccine; antiallergic; B cell epitope.
 XX
 OS Dermatophagoides pteronyssinus.
 OS Synthetic.
 OS WO200240676-A2.
 XX
 XX 23-MAY-2002.
 XX
 XX 16-NOV-2001; 2001WO-DK000764.
 XX
 PR 16-NOV-2000; 2000DK-00001718.
 PR 16-NOV-2000; 2000US-0249361P.
 PR 14-JUN-2001; 2001US-0298170P.
 XX
 XX (ALKA-) ALK-ABELLO AS.
 XX
 XX Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
 XX
 XX WPI; 2002-508328/54.
 XX N-PSDB; ABK95646.
 XX
 XX New recombinant mutant allergen, useful for preventing and/or treating
 PT allergy, comprises multiple mutations and reduced immunoglobulin E
 PT binding affinity.
 XX
 XX Example 7; Page; 210pp; English.
 XX
 XX The invention relates to a recombinant allergen (I) which is a mutant of
 CC a naturally occurring allergen, where the mutant allergen has at least
 CC four primary mutations, which each reduce the specific immunoglobulin E
 CC (IgE) binding capability of the mutated allergen as compared to the IgE
 CC binding capability of the naturally occurring allergen, where each
 CC primary mutation is a substitution of one surface-exposed amino acid
 CC residue with another residue, which does not occur in the same position
 CC in the amino acid sequence of any known homologous protein within the
 CC taxonomic species from which the naturally occurring allergen originates,
 CC and each primary mutation is spaced from each other primary mutation by
 CC at least 15 Angstrom , and the primary mutations are placed in such a
 CC manner that at least one circular surface region with a area of 800
 CC Angstrom ^2 comprises no mutation. Also included are a composition
 CC comprising two or more of the recombinant allergens, where the variant
 CC allergen is defined by having at least one primary mutation, which is
 CC absent in at least one of the other variants, and for each variant no
 CC secondary mutation is present within a radius of 15 Angstrom from each
 CC absent primary mutation; a DNA sequence encoding the recombinant allergen
 CC or its derivative, partial sequence or degenerated sequence, where the
 CC sequence which hybridises to it under stringent conditions, where the
 CC derivative, partial sequence, degenerated sequence or hybridising
 CC sequence encodes a peptide having at least one B cell epitope; an
 CC expression vector comprising the DNA and a host cell comprising the
 CC vector. The recombinant allergen is useful as a pharmaceutical, for
 CC preparing a pharmaceutical for preventing and/or treating allergy, or in
 CC a diagnostic assay for assessing relevance, safety or outcome of therapy
 CC of a subject, where an IgE containing sample of the subject is mixed with
 CC the recombinant allergen and assessed for the level of reactivity between
 CC the IgE in the sample and the recombinant allergen. The recombinant
 CC allergen or compositions are useful for generating an immune response in
 CC a subject, for vaccination or treatment of a subject or for the
 CC treatment, prevention or alleviation of allergic reactions in a subject
 CC e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
 CC anaphylaxis. The present sequence represents a recombinant allergen of
 CC the invention. Note: The present sequence was not shown in the
 CC specification but was created by the indexer using information in the
 CC specification and the corresponding wild-type sequence
 XX
 XX Sequence 222 AA;

Query Match 96.4%; Score 1162; DB 5; Length 222;
 Best Local Similarity 96.4%; Pred. No. 2.5e-122;

Matches 214; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TNACSGNAPAEIDLQRMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
 DB 1 TNACSGNAPAEIDLQRMQTVPIRMGGCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
 QY 61 ELVDCASQHCCHGDTIPRGIEYIQHNGVVQESYRYVAREQSCRRPNAQRFGLSNYCOIY 120
 DB 61 ELVDCANQHCCHGDTIPRGIEYIQHNGVVQESYRYVAREQSCRRPNAQRFGLSNYCOIY 120
 QY 121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIORNGYOPFNHAVNIVYSNA 180
 DB 121 PPNVANKIREALAQTHSAIAVIIGIKDLDAFRHYDGETIIQEDNGYQTNHAVNIVYSNA 180
 QY 181 QGVGYWIVRNSWDTNWGDNNGYGYFAANIDLMIMEEYPYVUIL 222
 DB 181 QGVGYWIVRNSWDTNWGDNNGYGYFAANIDLMIMEEYPYVUIL 222
 RESULT 13
 ABG67027
 ID ABG67027 standard; protein; 222 AA.
 XX
 XX AC ABG67027;
 XX
 XX DT 24-SEP-2002 (first entry)
 XX DE House dust mite allergen Der p 1 mutant #4.
 XX KW Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever;
 KW rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
 KW vaccine; antiallergic; B cell epitope.
 XX
 XX Dermatophagoides pteronyssinus.
 OS Synthetic.
 XX WO200240676-A2.
 XX
 XX 23-MAY-2002.
 XX
 XX 16-NOV-2001; 2001WO-DK000764.
 XX
 PR 16-NOV-2000; 2000DK-00001718.
 PR 16-NOV-2000; 2000US-0249361P.
 PR 14-JUN-2001; 2001US-0298170P.
 XX
 XX (ALKA-) ALK-ABELLO AS.
 XX
 XX Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
 XX
 XX WPI; 2002-508328/54.
 XX N-PSDB; ABK95643.
 XX
 XX New recombinant mutant allergen, useful for preventing and/or treating
 PT allergy, comprises multiple mutations and reduced immunoglobulin E
 PT binding affinity.
 XX
 XX Example 7; Page; 210pp; English.
 XX
 XX The invention relates to a recombinant allergen (I) which is a mutant of
 CC a naturally occurring allergen, where the mutant allergen has at least
 CC four primary mutations, which each reduce the specific immunoglobulin E
 CC (IgE) binding capability of the mutated allergen as compared to the IgE
 CC binding capability of the naturally occurring allergen, where each
 CC primary mutation is a substitution of one surface-exposed amino acid
 CC residue with another residue, which does not occur in the same position
 CC in the amino acid sequence of any known homologous protein within the
 CC taxonomic species from which the naturally occurring allergen originates,
 CC and each primary mutation is spaced from each other primary mutation by
 CC at least 15 Angstrom , and the primary mutations are placed in such a
 CC manner that at least one circular surface region with a area of 800
 CC Angstrom ^2 comprises no mutation. Also included are a composition
 CC comprising two or more of the recombinant allergens, where the variant
 CC allergen is defined by having at least one primary mutation, which is
 CC absent in at least one of the other variants, and for each variant no
 CC secondary mutation is present within a radius of 15 Angstrom from each
 CC absent primary mutation; a DNA sequence encoding the recombinant allergen
 CC or its derivative, partial sequence or degenerated sequence, where the
 CC sequence which hybridises to it under stringent conditions, where the
 CC derivative, partial sequence, degenerated sequence or hybridising
 CC sequence encodes a peptide having at least one B cell epitope; an
 CC expression vector comprising the DNA and a host cell comprising the
 CC vector. The recombinant allergen is useful as a pharmaceutical, for
 CC preparing a pharmaceutical for preventing and/or treating allergy, or in
 CC a diagnostic assay for assessing relevance, safety or outcome of therapy
 CC of a subject, where an IgE containing sample of the subject is mixed with
 CC the recombinant allergen and assessed for the level of reactivity between
 CC the IgE in the sample and the recombinant allergen. The recombinant
 CC allergen or compositions are useful for generating an immune response in
 CC a subject, for vaccination or treatment of a subject or for the
 CC treatment, prevention or alleviation of allergic reactions in a subject
 CC e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
 CC anaphylaxis. The present sequence represents a recombinant allergen of
 CC the invention. Note: The present sequence was not shown in the
 CC specification but was created by the indexer using information in the
 CC specification and the corresponding wild-type sequence
 XX
 XX Sequence 222 AA;

CC allergen is defined by having at least one primary mutation, which is
 CC absent in at least one of the other variants, and for each variant no
 CC secondary mutation is present within a radius of 15 Angstrom from each
 CC absent primary mutation; a DNA sequence encoding the recombinant allergen
 CC or its derivative, partial sequence or degenerated sequence, or a
 CC sequence which hybridises to it under stringent conditions, where the
 CC derivative, partial sequence, degenerated sequence or hybridising
 CC sequence encodes a peptide having at least one B cell epitope; an
 CC expression vector comprising the DNA and a host cell comprising the
 CC vector. The recombinant allergen is useful as a pharmaceutical, for
 CC preparing a pharmaceutical for preventing and/or treating allergy, or in
 CC a diagnostic assay for assessing relevance, safety or outcome of therapy
 CC of a subject, where an IGE containing sample of the subject is mixed with
 CC the recombinant allergen and assessed for the level of reactivity between
 CC the IGE in the sample and the recombinant allergen. The recombinant
 CC allergen or compositions are useful for generating an immune response in
 CC a subject, for vaccination or treatment of a subject or for the
 CC treatment, prevention or alleviation of allergic reactions in a subject
 CC e.g. hay fever, rhinoconjunctivitis, rhinitis, asthma or systemic
 CC anaphylaxis. The present sequence represents a recombinant allergen of
 CC the invention. Note: The present sequence was not shown in the
 CC specification but was created by the indexer using information in the
 CC specification and the corresponding wild-type sequence

XX Sequence 222 AA;

Query Match 96.3%; Score 1161; DB 5; Length 222;

Best Local Similarity 96.4%; Pred. No. 3.2e-122;

Matches 214; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 TNACSSINGNAPAEIDLROMETVTPIRMGGCGSCWAFSGVAATESAYLAHRNQSILDAEQ 60
 DB 1 TNACSSINGNAPAEIDLROMETVTPIRMGGCGSCWAFSGVAATESAYLAHRNQSILDAEQ 60
 QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
 DB 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
 QY 121 PPNAKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYSNA 180
 DB 121 PPNAKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYSNA 180
 QY 181 QGVDDYWIWRNSWDTNMGDNGYGYFAANIDLMIMIEEYPYVIL 222
 DB 181 QGVDDYWIWRNSWDTNMGDNGYGYFAANIDLMIMIEEYPYVIL 222

RESULT 14

ABG67029
 ID ABG67029 standard; protein; 222 AA.

XX AC ABG67029;

XX DT 24-SEP-2002 (first entry)

XX DE House dust mite allergen Der p 1 mutant #6.

XX KW Immunoglobulin E; IGE; allergen; allergy; mutein; hay fever;
 KW rhinoconjunctivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
 KW vaccine; antiallergic; B cell epitope.

XX OS Dermatoaphagoides pteronyssinus.
 OS Synthetic.

XX PN W0200240676-A2.

XX PD 23-MAY-2002.

XX PF 16-NOV-2001; 2001WO-DK000764.

XX PR 16-NOV-2000; 2000DK-00001718.

XX PR 16-NOV-2000; 2000US-0249361P.

XX PR 14-JUN-2001; 2001US-0298170P.

(ALKA-) ALK-ABELLO AS.

Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;

WPI; 2002-508328/54.

N-PSDB; ABK95645.

New recombinant mutant allergen, useful for preventing and/or treating
 allergy, comprises multiple mutations and reduced immunoglobulin E
 binding affinity.

Example 7; Page; 210pp; English.

The invention relates to a recombinant allergen (I) which is a mutant of
 a naturally occurring allergen, where the mutant allergen has at least
 four primary mutations, which each reduce the specific immunoglobulin E
 (IGE) binding capability of the mutated allergen as compared to the IGE
 binding capability of the naturally occurring allergen, where each
 primary mutation is a substitution of one surface-exposed amino acid
 residue with another residue, which does not occur in the same position
 in the amino acid sequence of any known homologous protein within the
 taxonomic species from which the naturally occurring allergen originates,
 and each primary mutation is spaced from each other primary mutation by
 at least 15 Angstrom, and the primary mutations are placed in such a
 manner that at least one circular surface region with a area of 800
 Angstrom² comprises no mutation. Also included are a composition
 comprising two or more of the recombinant allergens, where the variant
 allergen is defined by having at least one primary mutation, which is
 absent in at least one of the other variants, and for each variant no
 secondary mutation is present within a radius of 15 Angstrom from each
 absent primary mutation; a DNA sequence encoding the recombinant allergen
 or its derivative, partial sequence or degenerated sequence, or a
 sequence which hybridises to it under stringent conditions, where the
 derivative, partial sequence, degenerated sequence or hybridising
 sequence encodes a peptide having at least one B cell epitope; an
 expression vector comprising the DNA and a host cell comprising the
 vector. The recombinant allergen is useful as a pharmaceutical, for
 preparing a pharmaceutical for preventing and/or treating allergy, or in
 a diagnostic assay for assessing relevance, safety or outcome of therapy
 of a subject, where an IGE containing sample of the subject is mixed with
 the recombinant allergen and assessed for the level of reactivity between
 the IGE in the sample and the recombinant allergen. The recombinant
 allergen or compositions are useful for generating an immune response in
 a subject, for vaccination or treatment of a subject or for the
 treatment, prevention or alleviation of allergic reactions in a subject
 e.g. hay fever, rhinoconjunctivitis, rhinitis, asthma or systemic
 anaphylaxis. The present sequence represents a recombinant allergen of
 the invention. Note: the present sequence was not shown in the
 specification but was created by the indexer using information in the
 specification and the corresponding wild-type sequence

XX Sequence 222 AA;

Query Match 96.3%; Score 1161; DB 5; Length 222;

Best Local Similarity 96.4%; Pred. No. 3.2e-122;

Matches 214; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 TNACSSINGNAPAEIDLROMETVTPIRMGGCGSCWAFSGVAATESAYLAHRNQSILDAEQ 60
 DB 1 TNACSSINGNAPAEIDLROMETVTPIRMGGCGSCWAFSGVAATESAYLAHRNQSILDAEQ 60
 QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
 DB 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIY 120
 QY 121 PPNAKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYSNA 180
 DB 121 PPNAKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYSNA 180
 QY 181 QGVDDYWIWRNSWDTNMGDNGYGYFAANIDLMIMIEEYPYVIL 222
 DB 181 QGVDDYWIWRNSWDTNMGDNGYGYFAANIDLMIMIEEYPYVIL 222

RESULT 15
ABG67026
ID ABG67026 standard; protein; 222 AA.
XX AC ABG67026;
XX DT 24-SEP-2002 (first entry)
XX DE House dust mite allergen Der p 1 mutant #3.
XX KW Immunoglobulin E; IGE; allergen; allergy; mite; hay fever;
XX KM rhinoconjunctivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
XX KW vaccine; antiallergic; B cell epitope.
XX OS Dermatophagoides pteronyssinus.
OS Synthesis.
PN WC200240676-A2.
XX PD 23-MAY-2002.
XX PF 16-NOV-2001; 2001WO-DK000764.
XX PR 16-NOV-2000; 2000DK-00001718.
XX PR 16-NOV-2000; 2000US-0249361P.
XX PR 14-JUN-2001; 2001US-0298170P.
XX PA (ALKA-) ALK-ABELLO AS.
XX PI Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
XX WPI; 2002-508328/54.
XX DR N-PSDB; ABK95642.
XX PT New recombinant mutant allergen, useful for preventing and/or treating
XX PT allergy, comprises multiple mutations and reduced immunoglobulin E
XX PT binding affinity.
XX PS Example 7; Page; 210pp; English.
XX CC The invention relates to a recombinant allergen (I) which is a mutant of
XX CC a naturally occurring allergen, where the mutant allergen has at least
XX CC four primary mutations, which each reduce the specific immunoglobulin E
XX CC (IgE) binding capability of the mutated allergen as compared to the IgE
XX CC binding capability of the naturally occurring allergen, where each
XX CC primary mutation is a substitution of one surface-exposed amino acid
XX CC residue with another residue, which does not occur in the same position
XX CC in the amino acid sequence of any known homologous protein within the
XX CC taxonomic species from which the naturally occurring allergen originates,
XX CC and each primary mutation is spaced from each other primary mutation by
XX CC at least 15 Angstrom , and the primary mutations are placed in such a
XX CC manner that at least one circular surface region with a area of 800
XX CC Angstrom ^2 comprises no mutation. Also included are a composition
XX CC comprising two or more of the recombinant allergens, where the variant
XX CC allergen is defined by having at least one primary mutation, which is
XX CC absent in at least one of the other variants, and for each variant no
XX CC secondary mutation is present within a radius of 15 Angstrom from each
XX CC absent primary mutation; a DNA sequence encoding the recombinant allergen
XX CC or its derivative, partial sequence or degenerated sequence, or a
XX CC sequence which hybridises to it under stringent conditions, where the
XX CC derivative, partial sequence, degenerated sequence or hybridising
XX CC sequence encodes a peptide having at least one B cell epitope; an
XX CC expression vector comprising the DNA and a host cell comprising the
XX CC vector. The recombinant allergen is useful as a pharmaceutical, for
XX CC preparing a pharmaceutical for preventing and/or treating allergy, or in
XX CC a diagnostic assay for assessing relevance, safety or outcome of therapy
XX CC of a subject, where an IGE containing sample of the subject is mixed with
XX CC the recombinant allergen and assessed for the level of reactivity between
XX CC the IGE in the sample and the recombinant allergen. The recombinant
XX CC allergen or compositions are useful for generating an immune response in
XX CC a subject, for vaccination or treatment of a subject or for the

CC treatment, prevention or alleviation of allergic reactions in a subject
CC e.g. hay fever, rhinoconjunctivitis, rhinitis, asthma or systemic
CC anaphylaxis. The present sequence represents a recombinant allergen of
CC the invention. Note: The present sequence was not shown in the
CC specification but was created by the indexer using information in the
CC specification and the corresponding wild-type sequence
XX SQ Sequence 222 AA;
SQ Query Match 96.2%; Score 1160; DB 5; Length 222;
Best Local Similarity 96.4%; Pred. NO. 4.2e-122;
Matches 214; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 TNACSTNGNAPAEIDLROMRTVTPIRMGGCGSCWAFSGVAATESAYLAHNSLDLAEQ 60
DB 1 TNACSTNGNAPAEIDLROMRTVTPIRMGGCGSCWAFSGVAATESAYLAHNSLDLAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 120
DB 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGISNYCQIY 120
QY 121 PPNANKIREALAQTHSAIAVIGIKDLDAFRHYDGRITIQRDNGYQPNYHVNIVGYSNA 180
DB 121 PPNANKIREALAQTHSAIAVIGIKDLDAFRHYDGRITIQRDNGYQPNYHVNIVGYSNA 180
QY 181 QGVYDWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVIL 222
DB 181 QGVYDWIVRNSWDTNWDNGYGYFAANIDLMIEEYPYVIL 222

Search completed: May 19, 2005, 17:39:01
Job time : 163 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:36:23 ; Search time 135 Seconds
(without alignments)
550.079 Million cell updates/sec

Title: US-09-867-159A-2
Perfect score: 1206
Sequence: 1 TNACSSINGNAPAEIDLQMR.....YFAANIDLMIEBYPVVIL 222

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 893949

Minimum DB seq length: 0
Maximum DB seq length: 222

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1206	100.0	222	10	US-09-867-159A-2
2	1196	99.2	222	14	US-10-001-245-88
3	1162	96.4	222	14	US-10-001-245-26
4	1161	96.3	222	14	US-10-001-245-18
5	1161	96.3	222	14	US-10-001-245-20
6	1161	96.3	222	14	US-10-001-245-24
7	1160	96.2	218	17	US-10-892-543-5
8	1159	96.1	222	14	US-10-001-245-22
9	1157	95.9	222	14	US-10-001-245-14
10	1157	95.9	222	14	US-10-001-245-16
11	1143	94.8	222	14	US-10-001-245-30
12	1142	94.7	222	14	US-10-001-245-28
13	1133	93.9	222	14	US-10-001-245-34

14	1132	93.9	222	14	US-10-001-245-32	Sequence 32, Appl
15	982.5	81.5	211	10	US-09-847-208-95	Sequence 95, Appl
16	982.5	81.5	211	14	US-10-001-245-184	Sequence 184, App
17	944.5	78.3	210	14	US-10-001-245-185	Sequence 185, App
18	303	25.1	217	15	US-10-360-101-215	Sequence 215, App
19	297.5	24.7	218	11	US-09-972-211-90	Sequence 90, Appl
20	297.5	24.7	218	15	US-10-096-625-90	Sequence 90, Appl
21	294.5	24.4	220	11	US-09-972-211-89	Sequence 89, Appl
22	294.5	24.4	220	15	US-10-096-625-89	Sequence 89, Appl
23	282.5	23.4	210	16	US-10-466-110-7	Sequence 7, Appli
24	280.5	23.3	222	17	US-10-635-398-98	Sequence 98, Appl
25	278.5	23.1	217	14	US-10-273-577-5	Sequence 5, Appli
26	274	22.7	201	15	US-10-425-114-42955	Sequence 42955, A
27	271.5	22.5	217	14	US-10-273-577-2	Sequence 2, Appli
28	268.5	22.3	217	14	US-10-273-577-4	Sequence 4, Appli
29	261.5	21.7	217	14	US-10-273-577-3	Sequence 3, Appli
30	254	21.1	220	9	US-09-462-846-3	Sequence 3, Appli
31	254	21.1	220	16	US-10-773-387-3	Sequence 3, Appli
32	254	21.1	220	16	US-10-773-914-3	Sequence 3, Appli
33	251.5	20.9	200	14	US-10-219-220-150	Sequence 150, App
34	247	20.5	212	16	US-10-872-198-22	Sequence 22, Appl
35	247	20.5	212	17	US-10-872-197A-22	Sequence 22, Appl
36	235	19.5	205	15	US-10-425-114-53588	Sequence 53588, A
37	211	17.5	198	14	US-10-219-220-151	Sequence 151, App
38	208	17.2	129	14	US-10-219-220-159	Sequence 159, App
39	206	17.1	193	15	US-10-425-114-46437	Sequence 46437, A
40	205.5	17.0	195	16	US-10-767-701-43624	Sequence 43624, A
41	204	16.9	169	16	US-10-767-701-36832	Sequence 36832, A
42	201	16.7	147	14	US-10-219-220-173	Sequence 173, App
43	199.5	16.5	163	16	US-10-767-701-45098	Sequence 45098, A
44	197.5	16.4	160	14	US-10-219-220-155	Sequence 155, App
45	196	16.3	185	15	US-10-425-114-57524	Sequence 57524, A

ALIGNMENTS

RESULT 1

US-09-867-159A-2
; Sequence 2, Application US/09867159A
; Publication No. US20030104013A1
; GENERAL INFORMATION:
; APPLICANT: ANTIALIS TERRASSE, GAETAN LORIA, EMILE TREHIN, YVES
; TITLE OF INVENTION: Anti-allergic pharmaceutical composition containing at least one
; FILE REFERENCE: B112812US-antialis and at least one anti-histamine compound
; CURRENT FILING DATE: 2001-05-29
; PRIOR FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteromyssinus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(222)
; OTHER INFORMATION: Peptide sequence from cystine protease.
US-09-867-159A-2

Query Match 100.0%; Score 1206; DB 10; Length 222;
Best Local Similarity 100.0%; Pred. No 1.3e-118;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TNACSSINGNAPAEIDLQMRVTPIRMGGCGSWAFSGVAATESAYLAHRNQLDLAEQ 60
Db 1 TNACSSINGNAPAEIDLQMRVTPIRMGGCGSWAFSGVAATESAYLAHRNQLDLAEQ 60
Qy 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRPNQRFGISNYCQIY 120

Db 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGLSNYCQIY 120
QY 121 PPNANKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQDNGYQPNYHVNIVGYSNA 180
Db 121 PPNANKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQDNGYQPNYHVNIVGYSNA 180
QY 181 QGVYWIIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVUIL 222
Db 181 QGVYWIIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVUIL 222

RESULT 2

US-10-001-245-88
; Sequence 88, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-88

Query Match 99.2%; Score 1196; DB 14; Length 222;
Best Local Similarity 99.1%; Pred. No. 1.4e-117; Indels 0; Gaps 0;
Matches 220; Conservative 1; Mismatches 1;
QY 1 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
Db 1 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGLSNYCQIY 120
Db 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGLSNYCQIY 120
QY 121 PPNANKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQDNGYQPNYHVNIVGYSNA 180
Db 121 PPNANKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQDNGYQPNYHVNIVGYSNA 180
QY 181 QGVYWIIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVUIL 222
Db 181 QGVYWIIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVUIL 222

RESULT 3

US-10-001-245-86
; Sequence 26, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-26

Query Match 96.4%; Score 1162; DB 14; Length 222;
Best Local Similarity 96.4%; Pred. No. 5.5e-114;
Matches 214; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
Db 1 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGLSNYCQIY 120
Db 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGLSNYCQIY 120
QY 121 PPNANKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQDNGYQPNYHVNIVGYSNA 180
Db 121 PPNANKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQDNGYQPNYHVNIVGYSNA 180
QY 181 QGVYWIIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVUIL 222
Db 181 QGVYWIIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVUIL 222

RESULT 4

US-10-001-245-18
; Sequence 18, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-18

Query Match 96.3%; Score 1161; DB 14; Length 222;
Best Local Similarity 96.4%; Pred. No. 7e-114; Indels 0; Gaps 0;
Matches 214; Conservative 3; Mismatches 5;
QY 1 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
Db 1 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGLSNYCQIY 120
Db 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAQRFGLSNYCQIY 120
QY 121 PPNANKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQDNGYQPNYHVNIVGYSNA 180
Db 121 PPNANKIREALAQTHSAIAVIIGIKOLDAPRHYDGRITIIQDNGYQPNYHVNIVGYSNA 180
QY 181 QGVYWIIVRNSWDTNWDNGYGYFAANIDLMIMEEYPYVUIL 222

Db 181 QGVDTWIVRNSWDTNMGDNGYGYFAANIDLMIMEEYPYVWIL 222
|||||

RESULT 5

US-10-001-245-20
; Sequence 20, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1el mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-20

Query Match 96.3%; Score 1161; DB 14; Length 222;
Best Local Similarity 96.4%; Pred. No. 7e-114; Indels 0; Gaps 0;
Matches 214; Conservative 3; Mismatches 5;
Qy 1 TNACSSINGNAPAEIDLQRMETVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
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Db 1 TNACSSINGNAPAEIDLQRMETVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
|||
Qy 61 ELVDCASOHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCOIY 120
|||
Db 61 ELVDCASOHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCOIY 120
|||
Qy 121 PPANKIREALAOQTHSAIAVIIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYNSA 180
|||
Db 121 PPANKIREALAOQTHSAIAVIIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYNSA 180
|||
Qy 181 QGVDTWIVRNSWDTNMGDNGYGYFAANIDLMIMEEYPYVWIL 222
|||
Db 181 QGVDTWIVRNSWDTNMGDNGYGYFAANIDLMIMEEYPYVWIL 222
|||

RESULT 6

US-10-001-245-24
; Sequence 24, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1el mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus

US-10-001-245-24

Query Match 96.3%; Score 1161; DB 14; Length 222;
Best Local Similarity 96.4%; Pred. No. 7e-114; Indels 0; Gaps 0;
Matches 214; Conservative 2; Mismatches 6;
Qy 1 TNACSSINGNAPAEIDLQRMETVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
|||
Db 1 TNACSSINGNAPAEIDLQRMETVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
|||
Qy 61 ELVDCASOHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCOIY 120
|||
Db 61 ELVDCANQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCOIY 120
|||
Qy 121 PPANKIREALAOQTHSAIAVIIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYNSA 180
|||
Db 121 PPANKIREALAOQTHSAIAVIIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYNSA 180
|||
Qy 181 QGVDTWIVRNSWDTNMGDNGYGYFAANIDLMIMEEYPYVWIL 222
|||
Db 181 QGVDTWIVRNSWDTNMGDNGYGYFAANIDLMIMEEYPYVWIL 222
|||

RESULT 7

US-10-892-543-5
; Sequence 5, Application US/10892543
; Publication No. US20050053615A1
; GENERAL INFORMATION:
; APPLICANT: Best, Elaine A.
; APPLICANT: McDermott, Martin J.
; TITLE OF INVENTION: VARIANTS OF MITE GROUP 1 ALLERGENS FOR THE TREATMENT OF HOUSE
; FILE REFERENCE: AL-10
; CURRENT APPLICATION NUMBER: US/10/892,543
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: 60/487,812
; PRIOR FILING DATE: 2003-07-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-892-543-5

Query Match 96.2%; Score 1160; DB 17; Length 218;
Best Local Similarity 97.7%; Pred. No. 8.7e-114; Indels 4; Gaps 1;
Matches 217; Conservative 1; Mismatches 0;
Qy 1 TNACSSINGNAPAEIDLQRMETVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
|||
Db 1 TNACSSINGNAPAEIDLQRMETVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 56
|||
Qy 61 ELVDCASOHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCOIY 120
|||
Db 57 ELVDCASOHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRRPNAQRFGISNYCOIY 116
|||
Qy 121 PPANKIREALAOQTHSAIAVIIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYNSA 180
|||
Db 117 PPANKIREALAOQTHSAIAVIIGIKDLDAFRHYDGRITIIQDNGYQPNYHAVNIVGYNSA 176
|||
Qy 181 QGVDTWIVRNSWDTNMGDNGYGYFAANIDLMIMEEYPYVWIL 222
|||
Db 177 QGVDTWIVRNSWDTNMGDNGYGYFAANIDLMIMEEYPYVWIL 218
|||

RESULT 8

US-10-001-245-22
; Sequence 22, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik

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; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-22

Query Match          96.1%; Score 1159; DB 14; Length 222;
Best Local Similarity 96.4%; Pred. No. 1.1e-113;
Matches 214; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 TNACSGNAPAEIDLQRMRTVTPIRMQCGCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
DB 1 TNACSGNAPAEIDLQRMRTVTPIRMQCGCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYRYRYVAREQSCRRPNAQRFGISNYCQIY 120
DB 61 ELVDCANQHGCHGDTIPRGIEYIQHNGVVQESYRYRYVAREQSCRRPNAQRFGISNYCQIY 120
QY 121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
DB 121 PPNVKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQTNTHAVNIVGYSNA 180
QY 181 QGVYWIIVNSWDTNWGNDNGYGYFAANIDLMIMEEYPYVUIL 222
DB 181 QGVYWIIVNSWDTNWGNDNGYGYFAANIDLMIMEEYPYVUIL 222

RESULT 9
US-10-001-245-14
; Sequence 14, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-14

Query Match          95.9%; Score 1157; DB 14; Length 222;
Best Local Similarity 96.4%; Pred. No. 1.8e-113;
Matches 214; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 TNACSGNAPAEIDLQRMRTVTPIRMQCGCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
DB 1 TNACSGNAPAEIDLQRMRTVTPIRMQCGCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYRYRYVAREQSCRRPNAQRFGISNYCQIY 120
DB 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYRYRYVAREQSCRRPNAQRFGISNYCQIY 120
QY 121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
DB 121 PPNVKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQTNTHAVNIVGYSNA 180
QY 181 QGVYWIIVNSWDTNWGNDNGYGYFAANIDLMIMEEYPYVUIL 222
DB 181 QGVYWIIVNSWDTNWGNDNGYGYFAANIDLMIMEEYPYVUIL 222

RESULT 10
US-10-001-245-16
; Sequence 16, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-16

Query Match          95.9%; Score 1157; DB 14; Length 222;
Best Local Similarity 96.4%; Pred. No. 1.8e-113;
Matches 214; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 TNACSGNAPAEIDLQRMRTVTPIRMQCGCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
DB 1 TNACSGNAPAEIDLQRMRTVTPIRMQCGCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYRYRYVAREQSCRRPNAQRFGISNYCQIY 120
DB 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYRYRYVAREQSCRRPNAQRFGISNYCQIY 120
QY 121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
DB 121 PPNVKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQTNTHAVNIVGYSNA 180
QY 181 QGVYWIIVNSWDTNWGNDNGYGYFAANIDLMIMEEYPYVUIL 222
DB 181 QGVYWIIVNSWDTNWGNDNGYGYFAANIDLMIMEEYPYVUIL 222

RESULT 11
US-10-001-245-30
; Sequence 30, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14

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; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-22

Query Match          95.9%; Score 1157; DB 14; Length 222;
Best Local Similarity 96.4%; Pred. No. 1.8e-113;
Matches 214; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 TNACSGNAPAEIDLQRMRTVTPIRMQCGCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
DB 1 TNACSGNAPAEIDLQRMRTVTPIRMQCGCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYRYRYVAREQSCRRPNAQRFGISNYCQIY 120
DB 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYRYRYVAREQSCRRPNAQRFGISNYCQIY 120
QY 121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
DB 121 PPNVKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQTNTHAVNIVGYSNA 180
QY 181 QGVYWIIVNSWDTNWGNDNGYGYFAANIDLMIMEEYPYVUIL 222
DB 181 QGVYWIIVNSWDTNWGNDNGYGYFAANIDLMIMEEYPYVUIL 222

RESULT 10
US-10-001-245-16
; Sequence 16, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-16

Query Match          95.9%; Score 1157; DB 14; Length 222;
Best Local Similarity 96.4%; Pred. No. 1.8e-113;
Matches 214; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 TNACSGNAPAEIDLQRMRTVTPIRMQCGCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
DB 1 TNACSGNAPAEIDLQRMRTVTPIRMQCGCGSCWAFSGVAATESAYLAHRNQSLLAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYRYRYVAREQSCRRPNAQRFGISNYCQIY 120
DB 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYRYRYVAREQSCRRPNAQRFGISNYCQIY 120
QY 121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
DB 121 PPNVKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQTNTHAVNIVGYSNA 180
QY 181 QGVYWIIVNSWDTNWGNDNGYGYFAANIDLMIMEEYPYVUIL 222
DB 181 QGVYWIIVNSWDTNWGNDNGYGYFAANIDLMIMEEYPYVUIL 222

RESULT 11
US-10-001-245-30
; Sequence 30, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14

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; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-30

Query Match          94.8%; Score 1143; DB 14; Length 222;
Best Local Similarity 95.0%; Pred. No. 5.5e-112;
Matches 211; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
DB 1 TNACSSINGNAPASIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVQESYRYVAREQSCRRPNQAQFGISNYCQIY 120
DB 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVQESYRYVAREQSCRRPNQAQFGISNYCQIY 120
QY 121 PPVANKIEEALQTHSAIAVIIGIKDLDAFRHYDGRITIIQDDNGYQTNHVNIVGYNSA 180
DB 121 PPVANKIEEALQTHSAIAVIIGIKDLDAFRHYDGRITIIQDDNGYQTNHVNIVGYNSA 180
QY 181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMIEEYPYVIL 222
DB 181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMIEEYPYVIL 222

RESULT 12
US-10-001-245-28
; Sequence 28, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-28

Query Match          94.7%; Score 1142; DB 14; Length 222;
Best Local Similarity 95.0%; Pred. No. 7e-112;
Matches 211; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
DB 1 TNACSSINGNAPASIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVQESYRYVAREQSCRRPNQAQFGISNYCQIY 120
DB 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVQESYRYVAREQSCRRPNQAQFGISNYCQIY 120
QY 121 PPVANKIEEALQTHSAIAVIIGIKDLDAFRHYDGRITIIQDDNGYQTNHVNIVGYNSA 180
DB 121 PPVANKIEEALQTHSAIAVIIGIKDLDAFRHYDGRITIIQDDNGYQTNHVNIVGYNSA 180
QY 181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMIEEYPYVIL 222

RESULT 13
US-10-001-245-34
; Sequence 34, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-34

Query Match          93.9%; Score 1133; DB 14; Length 222;
Best Local Similarity 94.8%; Pred. No. 6.3e-111;
Matches 210; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
DB 1 TNACSSINGNAPASIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVQESYRYVAREQSCRRPNQAQFGISNYCQIY 120
DB 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVQESYRYVAREQSCRRPNQAQFGISNYCQIY 120
QY 121 PPVANKIEEALQTHSAIAVIIGIKDLDAFRHYDGRITIIQDDNGYQTNHVNIVGYNSA 180
DB 121 PPVANKIEEALQTHSAIAVIIGIKDLDAFRHYDGRITIIQDDNGYQTNHVNIVGYNSA 180
QY 181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMIEEYPYVIL 222
DB 181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMIEEYPYVIL 222

RESULT 14
US-10-001-245-32
; Sequence 32, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
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US-10-001-245-32

Query Match 93.9%; Score 1132; DB 14; Length 222;
Best Local Similarity 94.6%; Pred. No. 8e-111; 9; Indels 0; Gaps 0;
Matches 210; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 TNACSSINGNAPAEIDLQRMRTVTPIRMQGGSCSWAFSGVAATESAYLAHRNQSLLDLAEQ 60
DB 1 TNACSSINGNAPASIDLQRMRTVTPIRMQGGSCSWAFSGVAATESAYLAHRNQSLLDLAEQ 60

QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYRYVAREQSCRRPNAORFGISNYCQIY 120
DB 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYRYVAREQSCRRPNAORFGISNYCQIY 120

QY 121 PPNANKIREALQATHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
DB 121 PPNVKNIEBALQATHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180

QY 181 QGVVDYWIVRNSWDTNWGDNGYGYFAANIDLMIEEYPYVVIL 222
DB 181 QGVVDYWIVRNSWDTNWGDNGYGYFAANIDLMIEEYPYVVIL 222

RESULT 15

US-09-847-208-95
; Sequence 95, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Euroglyphus maynei (House-dust mite)
US-09-847-208-95

Query Match 81.5%; Score 982.5; DB 10; Length 211;
Best Local Similarity 83.9%; Pred. No. 4.3e-95;
Matches 177; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 TNACSSING-NAPAEIDLQRMRTVTPIRMQGGSCSWAFSGVAATESAYLAHRNQSLLDLAE 59
DB 1 TVACSSINSVSLPSELRLSLRTVTPIRMQGGSCSWAFSGVASTESAYLAHRNMSLLDLAE 60

QY 60 QELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYRYVAREQSCRRPNAORFGISNYCQI 119
DB 61 QELVDCASQHGCHGDTIPRGIEYIQHNGVQESYRYRYVAREQSCRRPNAORFGISNYCQI 120

QY 120 YPPNANKIREALQATHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGYSN 179
DB 121 SPSPSKIRKQALTQHTTAVAVIIGIKDLNFRHYDGRITIIQRDNGYQPNYHVNIVGYSN 180

QY 180 AQGVVDYWIVRNSWDTNWGDNGYGYFAANIDL 210
DB 181 TQGVVDYWIVRNSWDTNWGDNGYGYFAANINL 211

Search completed: May 19, 2005, 17:53:25
Job time : 136 secs

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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:31:52 ; Search time 22 Seconds
(without alignments)
753.277 Million cell updates/sec

Title: us-09-867-159a-2

Perfect score: 1206

Sequence: 1 TNACSGINGNAPAEIDLQMR.....YFAANIDLMIEBYPYVIL 222

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 402398

Minimum DB seq length: 0

Maximum DB seq length: 222

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgm2_6/ptodata/1/iaa/PTCUS_COMB.pep.*

6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1177	97.6	222	1	US-07-945-288-11
2	1177	97.6	222	1	US-08-462-831-11
3	1177	97.6	222	1	US-08-461-809-11
4	1177	97.6	222	1	US-08-461-441-11
5	1177	97.6	222	5	PCT-US93-08518-11
6	372.5	30.9	181	2	US-08-482-142-195
7	372.5	30.9	181	2	US-08-478-572-195
8	372.5	30.9	181	3	US-08-484-296-195
9	354.5	29.4	181	2	US-08-482-142-197
10	354.5	29.4	181	2	US-08-478-572-197
11	354.5	29.4	181	3	US-08-484-296-197
12	295	24.5	215	3	US-09-005-298-38
13	295	24.5	215	4	US-08-768-619-38
14	278	23.1	213	3	US-09-005-298-22
15	278	23.1	213	4	US-08-768-619-22
16	278	23.1	213	5	PCT-US96-09848-21
17	278	23.1	216	1	US-08-546-712-2
18	278	23.1	216	2	US-08-751-105-2
19	254	21.1	220	4	US-09-462-846-3
20	253	21.0	206	3	US-08-821-994-77
21	252	20.9	220	3	US-08-004-731-95
22	252	20.9	220	3	US-08-749-699-95
23	252	20.9	220	4	US-09-004-729-95
24	251.5	20.9	200	4	US-09-325-932A-150
25	248	20.6	215	1	US-08-451-409A-1
26	247	20.5	212	3	US-08-860-255A-4
27	239.5	19.9	213	2	US-08-578-701A-1

28	239.5	19.9	213	2	US-08-360-693-1	Sequence 1, Appli
29	238	19.7	181	2	US-08-482-142-193	Sequence 193, App
30	238	19.7	181	2	US-08-478-572-193	Sequence 193, App
31	238	19.7	181	3	US-08-484-296-193	Sequence 193, App
32	215.5	17.9	202	3	US-08-821-994-78	Sequence 78, Appl
33	211	17.5	198	4	US-09-325-932A-151	Sequence 151, App
34	208	17.2	129	4	US-09-325-932A-159	Sequence 159, App
35	201	16.7	147	4	US-09-325-932A-173	Sequence 173, App
36	197.5	16.4	160	4	US-09-325-932A-155	Sequence 155, App
37	195	16.2	204	4	US-09-325-932A-145	Sequence 145, App
38	181	15.0	130	4	US-09-325-932A-164	Sequence 164, App
39	175.5	14.6	157	4	US-08-424-361B-17	Sequence 17, Appl
40	174	14.4	168	3	US-08-821-994-45	Sequence 45, Appl
41	173	14.3	29	2	US-08-482-142-39	Sequence 39, Appl
42	173	14.3	29	2	US-08-478-572-39	Sequence 39, Appl
43	173	14.3	29	3	US-08-484-296-39	Sequence 39, Appl
44	172	14.3	119	4	US-09-325-932A-168	Sequence 168, App
45	167	13.8	167	3	US-08-821-994-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1

US-07-945-288-11

; Sequence 11, Application US/07945288

; Patent No. 5433948

; GENERAL INFORMATION:

; APPLICANT: Thomas, Wayne R.

; APPLICANT: Chua, Kaw-Yan

; TITLE OF INVENTION: CLONING AND SEQUENCING OF ALLERGENS FROM

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 STATE STREET, SUITE 510

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII TEXT

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/945,288

; FILING DATE: 19920910

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 580,655

; FILING DATE: 11 SEPTEMBER 1990

; APPLICATION NUMBER: 458,642

; FILING DATE: 13 FEBRUARY 1990

; ATTORNEY/AGENT INFORMATION:

; NAME: MANDRAGOURAS, AMY E.

; REGISTRATION NUMBER: P36,207

; REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 222 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: 50

; OTHER INFORMATION: /label-xaa is His or Tyr

; FEATURE:

; NAME/KEY: misc feature

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; LOCATION: 81
; OTHER INFORMATION: /label=Xaa is Glu or Lys
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 124
; OTHER INFORMATION: /label=Xaa is Ala or Val
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 136
; OTHER INFORMATION: /label=Xaa is Ser or Thr
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 215
; OTHER INFORMATION: /label=Xaa is Glu or Gln
; US-07-945-288-11

Query Match          97.6%; Score 1177; DB 1; Length 222;
Best Local Similarity 97.7%; Pred. No. 2.5e-126;
Matches 217; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TNACSGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
DB 1 TNACSGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAORFGISNYCQIY 120
DB 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAORFGISNYCQIY 120
QY 121 PPNANKIREALAQTHSAIAIIVIGIKDAPRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
DB 121 PPNANKIREALAQTHSAIAIIVIGIKDAPRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
QY 181 QGVYDWIVRNSWDTNWDNGYGYFAANIDLMIMIEEYPYVVIL 222
DB 181 QGVYDWIVRNSWDTNWDNGYGYFAANIDLMIMIEEYPYVVIL 222

RESULT 2
US-08-462-831-11
; Sequence 11, Application US/08462831
; Patent No. 5552142
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
; TITLE OF INVENTION: DERMATOPHAGOIDES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,831
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/945,288
; FILING DATE: 10 SEPTEMBER 1992
; APPLICATION NUMBER: US 580,655
; FILING DATE: 11 SEPTEMBER 1990
; APPLICATION NUMBER: US 458,642
; FILING DATE: 13 FEBRUARY 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDRAGOURAS, AMY E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 50
; OTHER INFORMATION: /label=Xaa is His or Tyr
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 81
; OTHER INFORMATION: /label=Xaa is Glu or Lys
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 124
; OTHER INFORMATION: /label=Xaa is Ala or Val
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 136
; OTHER INFORMATION: /label=Xaa is Ser or Thr
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 215
; OTHER INFORMATION: /label=Xaa is Glu or Gln
; US-08-462-831-11

Query Match          97.6%; Score 1177; DB 1; Length 222;
Best Local Similarity 97.7%; Pred. No. 2.5e-126;
Matches 217; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TNACSGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
DB 1 TNACSGNAPAEIDLQRMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAORFGISNYCQIY 120
DB 61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAREQSCRRPNAORFGISNYCQIY 120
QY 121 PPNANKIREALAQTHSAIAIIVIGIKDAPRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
DB 121 PPNANKIREALAQTHSAIAIIVIGIKDAPRHYDGRITIIQRDNGYQPNYHVNIVGYSNA 180
QY 181 QGVYDWIVRNSWDTNWDNGYGYFAANIDLMIMIEEYPYVVIL 222
DB 181 QGVYDWIVRNSWDTNWDNGYGYFAANIDLMIMIEEYPYVVIL 222

RESULT 3
US-08-461-809-11
; Sequence 11, Application US/08461809
; Patent No. 5770202
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
; TITLE OF INVENTION: DERMATOPHAGOIDES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,809
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/945,288
; FILING DATE: 10 SEPTEMBER 1992
; APPLICATION NUMBER: US 580,655
; FILING DATE: 11 SEPTEMBER 1990
; APPLICATION NUMBER: US 458,642
; FILING DATE: 13 FEBRUARY 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDRAGOURAS, AMY E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 50
; OTHER INFORMATION: /label=Xaa is His or Tyr
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 81
; OTHER INFORMATION: /label=Xaa is Glu or Lys
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 124
; OTHER INFORMATION: /label=Xaa is Ala or Val
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 136
; OTHER INFORMATION: /label=Xaa is Ser or Thr
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 215
; OTHER INFORMATION: /label=Xaa is Glu or Gln
; US-08-461-809-11

Query Match 97.6%; Score 1177; DB 1; Length 222;
Best Local Similarity 97.7%; Pred. No. 2.5e-126;
Matches 217; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TNACSSINGNAPAEIDLQRMETVTPIRMGGCGSCWAFSGVAATESAYLAHRNQSLLDAEQ 60
DB 1 TNACSSINGNAPAEIDLQRMETVTPIRMGGCGSCWAFSGVAATESAYLAHRNQSLLDAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNQVVOESYRYVAREQSCRRPNQAFGISNYCQIY 120
DB 61 ELVDCASQHGCHGDTIPRGIEYIQHNQVVOESYRYVAREQSCRRPNQAFGISNYCQIY 120
QY 121 PPANKIREALQTHSAIAVLIGIKLDAPRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 180
DB 121 PPANKIREALQTHSAIAVLIGIKLDAPRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 180
QY 181 QGVVDYWIVRNSWDTNMGDNGYGFPAANIDLMWIEEYFVVIL 222
DB 181 QGVVDYWIVRNSWDTNMGDNGYGFPAANIDLMWIEEYFVVIL 222

RESULT 4
US-08-461-441-11
; Sequence 11, Application US/08461441
; Patent No. 5773002
; GENERAL INFORMATION:
; APPLICANT:

; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
; TITLE OF INVENTION: DERMATOPHAGOIDES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,441
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/945,288
; FILING DATE: 10 SEPTEMBER 1992
; APPLICATION NUMBER: US 580,655
; FILING DATE: 11 SEPTEMBER 1990
; APPLICATION NUMBER: US 458,642
; FILING DATE: 13 FEBRUARY 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDRAGOURAS, AMY E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 50
; OTHER INFORMATION: /label=Xaa is His or Tyr
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 81
; OTHER INFORMATION: /label=Xaa is Glu or Lys
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 124
; OTHER INFORMATION: /label=Xaa is Ala or Val
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 136
; OTHER INFORMATION: /label=Xaa is Ser or Thr
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 215
; OTHER INFORMATION: /label=Xaa is Glu or Gln
; US-08-461-441-11

Query Match 97.6%; Score 1177; DB 1; Length 222;
Best Local Similarity 97.7%; Pred. No. 2.5e-126;
Matches 217; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TNACSSINGNAPAEIDLQRMETVTPIRMGGCGSCWAFSGVAATESAYLAHRNQSLLDAEQ 60
DB 1 TNACSSINGNAPAEIDLQRMETVTPIRMGGCGSCWAFSGVAATESAYLAHRNQSLLDAEQ 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIQHNQVVOESYRYVAREQSCRRPNQAFGISNYCQIY 120
DB 61 ELVDCASQHGCHGDTIPRGIEYIQHNQVVOESYRYVAREQSCRRPNQAFGISNYCQIY 120
QY 121 PPANKIREALQTHSAIAVLIGIKLDAPRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 180
DB 121 PPANKIREALQTHSAIAVLIGIKLDAPRHYDGRITIIQDNGYQPNYHAVNIVGYSNA 180
QY 181 QGVVDYWIVRNSWDTNMGDNGYGFPAANIDLMWIEEYFVVIL 222
DB 181 QGVVDYWIVRNSWDTNMGDNGYGFPAANIDLMWIEEYFVVIL 222
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QY 121 PPNANKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQDRNGYQPNYHNAVNIYGYSNA 180
Db 121 PPNXNKIREALQTHXAIAVIIGIKDLDAFRHYDGRITIIQDRNGYQPNYHNAVNIYGYSNA 180
QY 181 QGVYDWIVRNSWDTNWGNGYGYFAANIDLMMEIEYPPYVIL 222
Db 181 QGVYDWIVRNSWDTNWGNGYGYFAANIDLMMEIEYPPYVIL 222

RESULT 5

PCT-US93-08518-11
; Sequence 11, Application PC/TUS9308518
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION NUMBER: PCT/US93/08518
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/945,288
; FILING DATE: 10 SEPTEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDRAGOURAS, AMY E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 50
; OTHER INFORMATION: /label=Xaa is His or Tyr
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 81
; OTHER INFORMATION: /label=Xaa is Glu or Lys
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 124
; OTHER INFORMATION: /label=Xaa is Ala or Val
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 136
; OTHER INFORMATION: /label=Xaa is Ser or Thr
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 215
; OTHER INFORMATION: /label=Xaa is Glu or Gln
PCT-US93-08518-11

Query Match 97.6%; Score 1177; DB 5; Length 222;
Best Local Similarity 97.7%; Pred. No. 2.5e-126;

Matches 217; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 TNACSGINGNAPAEIDLROMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEO 60
Db 1 TNACSGINGNAPAEIDLROMRTVTPIRMGGCGSCWAFSGVAATESAYLAHRNOSLDLAEO 60
QY 61 ELVDCASQHGCHGDTIPRGIEYIOHNGVVOESYRYVAREQSCRPNQORFGISNYCQIY 120
Db 61 ELVDCASQHGCHGDTIPRGIXYIQHNGVVOESYRYVAREQSCRPNQORFGISNYCQIY 120
QY 121 PPNANKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQDRNGYQPNYHNAVNIYGYSNA 180
Db 121 PPNXNKIREALQTHXAIAVIIGIKDLDAFRHYDGRITIIQDRNGYQPNYHNAVNIYGYSNA 180
QY 181 QGVYDWIVRNSWDTNWGNGYGYFAANIDLMMEIEYPPYVIL 222
Db 181 QGVYDWIVRNSWDTNWGNGYGYFAANIDLMMEIEYPPYVIL 222

RESULT 6

US-08-482-142-195
; Sequence 195, Application US/08482142
; Patent No. 5820862
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-Chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,142
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,307
; FILING DATE: 07 June 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.6US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 195:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-142-195

Query Match 30.9%; Score 372.5; DB 2; Length 181;
Best Local Similarity 62.6%; Pred. No. 2.2e-34;
Matches 82; Conservative 8; Mismatches 14; Indels 27; Gaps 4;

QY 40 VAATESAYLAHRNQSLLDARQELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAR 99
Db 24 VAATESAYLAHRNTSLDSEQLVD-----EYIQHNGVVOESYRYVAR 67
QY 100 EQSCRRPNAQRFISNYCQIYPPNAN---KIREALAQTHSAJAVIIGIKDLDAFRHYDG 155
Db 68 EQSCRRPNAQLE-----AVFEANQNTKTAKIE--IKASIDGLGLEVIIGIKDLDAFRHYDG 120
QY 156 RTIIQRDNGYQ 166
Db 121 RTIIQRDNGYQ 131

RESULT 7
US-08-478-572-195
; Sequence 195, Application US/08478572
; Patent No. 5968526
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,572
; FILING DATE: 07-June-1995
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/445,307
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.6US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 195:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-478-572-195

Query Match 30.9%; Score 372.5; DB 2; Length 181;
Best Local Similarity 62.6%; Pred. No. 2.2e-34;
Matches 82; Conservative 8; Mismatches 14; Indels 27; Gaps 4;

QY 40 VAATESAYLAHRNQSLLDARQELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAR 99
Db 24 VAATESAYLAHRNTSLDSEQLVD-----EYIQHNGVVOESYRYVAR 67
QY 100 EQSCRRPNAQRFISNYCQIYPPNAN---KIREALAQTHSAJAVIIGIKDLDAFRHYDG 155
Db 68 EQSCRRPNAQLE-----AVFEANQNTKTAKIE--IKASIDGLGLEVIIGIKDLDAFRHYDG 120

Db 68 EQSCRRPNAQLE-----AVFEANQNTKTAKIE--IKASIDGLGLEVIIGIKDLDAFRHYDG 120
QY 156 RTIIQRDNGYQ 166
Db 121 RTIIQRDNGYQ 131

RESULT 8
US-08-484-296-195
; Sequence 195, Application US/08484296
; Patent No. 6268491
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,296
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/445,307
; FILING DATE: 07 June 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.6US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 195:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-296-195

Query Match 30.9%; Score 372.5; DB 3; Length 181;
Best Local Similarity 62.6%; Pred. No. 2.2e-34;
Matches 82; Conservative 8; Mismatches 14; Indels 27; Gaps 4;

QY 40 VAATESAYLAHRNQSLLDARQELVDCASQHGCHGDTIPRGIEYIQHNGVVOESYRYVAR 99
Db 24 VAATESAYLAHRNTSLDSEQLVD-----EYIQHNGVVOESYRYVAR 67
QY 100 EQSCRRPNAQRFISNYCQIYPPNAN---KIREALAQTHSAJAVIIGIKDLDAFRHYDG 155
Db 68 EQSCRRPNAQLE-----AVFEANQNTKTAKIE--IKASIDGLGLEVIIGIKDLDAFRHYDG 120
QY 156 RTIIQRDNGYQ 166
Db 121 RTIIQRDNGYQ 131

RESULT 9

US-08-482-142-197
; Sequence 197, Application US/08482142
; Patent No. 5820862
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; FILING DATE: 07 June 1995
; APPLICATION NUMBER: US/08/482,142
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,307
; FILING DATE: 07 June 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.6US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 197:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-142-197

Query Match 29.4%; Score 354.5; DB 2; Length 181;
Best Local Similarity 48.8%; Pred. No. 2.6e-32;
Matches 79; Conservative 0; Mismatches 0; Indels 83; Gaps 2;
QY 5 SINGNAPAEIDLQMRVTPIRMGGCGSWAFSGVAATESAYLAHRNQLDLAEQELVD 64
Db 24 SINGNAPAEIDLQMRVTPIRMQ----- 47
QY 65 CASQHGCHGDTTPRGLEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIYPPNA 124
Db 48 -----EYIQHNGVQESYRYVAREQSCRRPNAQ----- 76
QY 125 NKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQDNGYQ 166
Db 77 -----IIGIKDLDAFRHYDGRITIIQDNGYQ 102

RESULT 10

US-08-478-572-197
; Sequence 197, Application US/08478572
; Patent No. 5968526
; GENERAL INFORMATION:

; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; FILING DATE: 07-June-1995
; APPLICATION NUMBER: US/08/478,572
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/445,307
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.6US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 197:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-478-572-197

Query Match 29.4%; Score 354.5; DB 2; Length 181;
Best Local Similarity 48.8%; Pred. No. 2.6e-32;
Matches 79; Conservative 0; Mismatches 0; Indels 83; Gaps 2;
QY 5 SINGNAPAEIDLQMRVTPIRMGGCGSWAFSGVAATESAYLAHRNQLDLAEQELVD 64
Db 24 SINGNAPAEIDLQMRVTPIRMQ----- 47
QY 65 CASQHGCHGDTTPRGLEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIYPPNA 124
Db 48 -----EYIQHNGVQESYRYVAREQSCRRPNAQ----- 76
QY 125 NKIREALQTHSAIAVIIGIKDLDAFRHYDGRITIIQDNGYQ 166
Db 77 -----IIGIKDLDAFRHYDGRITIIQDNGYQ 102

RESULT 11

US-08-484-296-197
; Sequence 197, Application US/08484296
; Patent No. 6286491
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian

RESULT 12
 US-09-005-298-38
 ; Sequence 38, Application US/09005298
 ; Patent No. 6365392
 ; GENERAL INFORMATION:
 ; APPLICANT: Tripp, Cynthia A.
 ; APPLICANT: Wisniewski, Nancy
 ; APPLICANT: Grieve, Robert B.
 ; APPLICANT: Frank, Glenn R.
 ; TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTINE
 ; TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
 ; NUMBER OF SEQUENCES: 46
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sheridan Ross P.C.
 ; STREET: 1700 Lincoln Street, Suite 3500
 ; CITY: Denver
 ; STATE: Colorado

RESULT 13
US-08-768-619-38
; Sequence 38, Application US/08768619
; Patent No. 6419923
; GENERAL INFORMATION:
; APPLICANT: Tripp, Cynthia A.
; APPLICANT: Wisniewski, Nancy
; APPLICANT: Grieve, Robert B.
; APPLICANT: Frank, Glenn R.
; TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE
; TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,619
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,036
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-33-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-768-619-38

Query Match 24.5%; Score 295; DB 4; Length 215;
Best Local Similarity 35.8%; Pred. No. 2.2e-25;
Matches 73; Conservative 30; Mismatches 89; Indels 12; Gaps 7;
QY 11 PAEIDLROMRTVTPIRMQGGSCSWAFSGVAATESAYLAHRNOSLDLAQELVDCA---S 67
DB 2 PKYDWRKRGYVTPAKEQGLCGSCYAFCAAAALEAYNKKTKNKLKLDLSPQNLDCDCTWDLG 61
QY 68 QHCHGCDTIPRGIEYIOHNGVVOESYRYV--AREQSCRRPNAQRFGISNYCOIYPPNAN 125
DB 62 NNGCHGGFNPAPFYASKAGIASIAKYPVHTARTCTYWRKDIVAATDNGYTRIQQGDEK 121
QY 126 KIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGY--SNAQGV 183
DB 122 GLQYAVAKFGPVVVGISGQ--HDFKFKYS-GVYSSDQCRVFN-HAVLVVGYGTSKKHG- 176
QY 184 DYWIVRNSWDTNWGDNGYGYFAAN 207
DB 177 DYWIINKSWGNTWNGRNGYGYMKRN 200

RESULT 14
US-09-005-298-22
Sequence 22, Application US/09005298
Patent No. 6365392
GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
APPLICANT: Wisniewski, Nancy
APPLICANT: Grieve, Robert B.
APPLICANT: Frank, Glenn R.
TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE
TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,298
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/768,619
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-33-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-298-22

Query Match 23.1%; Score 278; DB 3; Length 213;
Best Local Similarity 34.8%; Pred. No. 1.9e-23;
Matches 71; Conservative 27; Mismatches 92; Indels 14; Gaps 8;
QY 11 PAEIDLROMRTVTPIRMQGGSCSWAFSGVAATESAYLAHRNOSLDLAQELVDCA---S 67
DB 2 PKYDWRKRGYVTPAKEQGLCGSCYAFCAAAALEAYNKKTKNKLKLDLSPQNLDCDCTWDLG 61
QY 68 QHCHGCDTIPRGIEYIOHNGVVOESYRYV--AREQSCRRPNAQRFGISNYCOIYPPNAN 125
DB 62 NNGCHGGFNPAPFYASKAGIASIAKYPVHTARTCTYWRKDIVAATDNGYTRIQQGD-E 120
QY 126 KIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHVNIVGY--SNAQGV- 183
DB 121 KGLNLMQ----LTVVVGISGYQHDFFKFKYS-GVYSSDQCRVFN-HAVLVVGYGTSQKTR 174
QY 184 DYWIVRNSWDTNWGDNGYGYFAAN 207
DB 175 DYWIINKSWGNTWNGRNGYGYMKRN 198

RESULT 15
US-08-768-619-22
Sequence 22, Application US/08768619
Patent No. 6419923
GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
APPLICANT: Wisniewski, Nancy
APPLICANT: Grieve, Robert B.
APPLICANT: Frank, Glenn R.
TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE
TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,619
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,036
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020

; REFERENCE/DOCKET NUMBER: 2618-33-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-768-619-22

Query Match 23.1%; Score 278; DB 4; Length 213;
Best Local Similarity 34.8%; Pred. No. 1.9e-23;
Matches 71; Conservative 27; Mismatches 92; Indels 14; Gaps 8;
QY 11 PAETDLQMRVTPIRMQGGCGSWAFSGVAATESAYLAHRNQSLLDAEQELVDCA---S 67
Db 2 PKYDWRKRGVYTPAKEQGLCGSCYAFCSCSIRSLIYKTKNKLDDLPQNILDCTWDLG 61
QY 68 QHGCHGDTIPRGIEYIOHNGVVOESYRYV--AREQSCRPNQAFGISNYCQIYPNPAN 125
Db 62 NNGCHGGFMNPAFYASKAGIASEAKYPYVHTARTCYWRKDIVAATDNGYTRIQQGD-E 120
QY 126 KIREALAQTHSAIAVIIIGIKOLD-APRHYDGRITIIQRDNGYQPNYHAWNIVGYSNAQGV- 183
Db 121 KGLNMLWQ----LTVVVGISGYQHDFFKYS-GVYSSDQCRVPN-HAVLVVVGYSOKTR 174
QY 184 DYWIVRNSWDTNMGDNGYGYFAAN 207
Db 175 DYWIIKNSWGINWARNGYGTWKRN 198

Search completed: May 19, 2005, 17:36:14
Job time : 24 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:50:19 ; Search time 12 Seconds
(without alignments)
80.181 Million cell updates/sec

Title: US-09-867-159A-3
Perfect score: 61
Sequence: 1 RMQGGCGSCN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	21	34.4	10	2 S70336	napiin small chain
2	20	32.8	7	2 A12016	formylglycinamide
3	19	31.1	9	2 I50633	c-rel protein - ch
4	19	31.1	10	2 D61440	polysialacturonase
5	19	31.1	10	2 Z27873	hypothetical prote
6	18	29.5	9	1 YFPG	thymic factor - pi
7	18	29.5	9	2 A60957	thymocyte growth p
8	18	29.5	10	2 A61289	streptopain (EC 3.
9	17	27.9	3	3 A23751	spinal cord peptid
10	17	27.9	6	2 P70727	i-cell receptor be
11	17	27.9	10	2 S06964	hypothetical prote
12	17	27.9	10	2 A60527	sperm-activating p
13	17	27.9	10	2 H60787	sperm-activating p
14	17	27.9	10	2 F60787	sperm-activating p
15	17	27.9	10	2 A60787	sperm-activating p
16	17	27.9	10	2 D60787	sperm-activating p
17	17	27.9	10	2 B60787	sperm-activating p
18	17	27.9	10	2 D60588	sperm-activating p
19	17	27.9	10	2 B60588	sperm-activating p
20	17	27.9	10	2 C60588	sperm-activating p
21	17	27.9	10	2 F60527	sperm-activating p
22	17	27.9	10	2 A60588	sperm-activating p
23	17	27.9	10	2 A60788	sperm-activating p
24	17	27.9	10	2 D60527	sperm-activating p
25	17	27.9	10	2 C39572	sperm-activating p
26	17	27.9	10	2 F60527	sperm-activating p
27	17	27.9	10	2 C60527	sperm-activating p
28	17	27.9	10	2 B60527	sperm-activating p
29	17	27.9	10	2 G60527	sperm-activating p

30	17	27.9	10	2 E39572	sperm-activating p
31	17	27.9	10	2 D60788	sperm-activating p
32	17	27.9	10	2 B60788	sperm-activating p
33	17	27.9	10	2 C60788	sperm-activating p
34	17	27.9	10	2 F60589	sperm-activating p
35	17	27.9	10	2 C60589	sperm-activating p
36	17	27.9	10	2 D60589	sperm-activating p
37	17	27.9	10	2 F60588	sperm-activating p
38	17	27.9	10	2 B60589	sperm-activating p
39	16	26.2	5	2 F22565	R-phycoerythrin ga
40	16	26.2	6	4 I79564	hypothetical TCU3
41	16	26.2	10	2 S51912	hemagglutinin - in
42	16	26.2	10	2 A35356	hypothetical prote
43	16	26.2	10	2 B61440	polysialacturonase
44	15	24.6	4	2 S47552	ubiquitin - rat
45	15	24.6	5	2 A33882	cadmium-binding pe

ALIGNMENTS

RESULT 1

S70336

napiin small chain S1A - Swedish turnip (fragment)

C;Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)

C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004

C;Accession: S70336

R;Neumann, G.M.; Condron, R.; Thomas, I.; Polya, G.M.

Biochim. Biophys. Acta 1295, 23-33, 1996

A;Title: Purification and sequencing of multiple forms of Brassica napus seed napin smal

A;Reference number: S70336; MUID:96283790; PMID:8679670

A;Accession: S70336

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <NEU>

A;Cross-references: UNIPROT:Q42469; UNIPROT:Q9S9F2

Query Match 34.4%; Score 21; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 3.6e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 MQSGCG 7

Db 3 MQSGSG 8

RESULT 2

Al2016

formylglycinamide ribonucleotide amidotransferase (EC 2.-.-.-) - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1997

C;Accession: A12016; B12016

R;Ohnoki, S.; Hong, B.S.; Buchanan, J.M.

Fed. Proc. 35, 1549, 1976

A;Title: Amino acid sequence at glutamine active site for FGAR-amidotransferase.

A;Reference number: A91459

A;Accession: A12016

A;Molecule type: protein

A;Residues: 1-7 <OHN>

A;Experimental source: liver, peptide 1

A;Accession: B12016

A;Molecule type: protein

A;Residues: 1-5 <OH2>

A;Experimental source: liver, peptide 2

C;Keywords: transferase

Query Match 32.8%; Score 20; DB 2; Length 7;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GGCGSC 9

Db 1 GVCDBC 6

RESULT 3
 I50633
 c-rel protein - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: I50633
 R:Hannink, M.; Temin, H.M.
 Oncogene 5, 1843-1850, 1990
 A:Title: Structure and autoregulation of the c-rel promoter.
 A:Reference number: I50633; MUID:91133738; PMID:2284104
 A:Accession: I50633
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-9 <HAN>
 A:Cross-references: UNIPROT:Q92009; EMBL:X56440; NID:g63338; PIDN:CAA39822.1; PID:g58448

 Query Match 31.1%; Score 19; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 QY 2 MQGGCG 7
 : |||
 Db 3 VSGGAG 8

 RESULT 4
 D61440
 polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)
 C:Species: Aspergillus sp.
 C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
 C:Accession: D61440
 R:Stratilova, E.; Markovic, O.; Skrovinova, D.; Rexova-Benkova, L.; Jorvall, H.
 J. Protein Chem. 12, 15-22, 1993
 A:Title: Pectinase Aspergillus sp. polygalacturonase: multiplicity, divergence, and structure.
 A:Reference number: A61440; MUID:93151962; PMID:8427629
 A:Accession: D61440
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <STR>
 A:Cross-references: UNIPROT:Q7M501
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

 Query Match 31.1%; Score 19; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 7 GSC 9
 : |||
 Db 1 GSC 3

 RESULT 5
 S27873
 hypothetical protein 2 LRH-1 5'-region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
 C:Accession: S27873
 R:Tugwood, J.D.; Issemann, I.; Green, S.
 submitted to the EMBL Data Library, February 1992
 A:Description: LRH-1: A nuclear hormone receptor active in the absence of exogenous ligand
 A:Reference number: S27873
 A:Accession: S27873
 A:Molecule type: mRNA
 A:Residues: 1-10 <TUG>
 A:Cross-references: UNIPROT:Q61807; EMBL:M81385; NID:g198872; PIDN:AAA39446.1; PID:g1988

 Query Match 31.1%; Score 19; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 8 SCN 10

Db 3 SCN 5

 RESULT 6
 YFPG
 thymic factor - pig
 N:Alternate names: FTS (facteur thymique serique)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
 C:Accession: A01523; A60983
 R:Pleau, J.M.; Dardenne, M.; Blouquit, Y.; Bach, J.F.
 J. Biol. Chem. 252, 8045-8047, 1977
 A:Title: Structural study of circulating thymic factor: a peptide isolated from pig serum
 A:Reference number: A01523; MUID:78026571; PMID:914862
 A:Accession: A01523
 A:Molecule type: protein
 A:Residues: 1-9 <PLE>
 A:Cross-references: UNIPROT:P01255
 R:Bach, J.F.; Dardenne, M.; Pleau, J.M.; Rosa, J.
 Nature 266, 55-57, 1977
 A:Title: Biochemical characterisation of a serum thymic factor.
 A:Reference number: A60983; MUID:77123829; PMID:300146
 A:Accession: A60983
 A:Molecule type: protein
 A:Residues: 'Z', 2-4, 'Z', 6-9 <BAC>
 A:Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral
 in a variety of immunoassays.
 C:Comment: See PIR:A60957 (sheep) for discussion of another possible N-terminal modification
 C:Superfamily: thymic factor
 C:Keywords: pyrrolidone carboxylic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

 Query Match 29.5%; Score 18; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 1 RMQGG 5
 : |||
 Db 3 KSQGG 7

 RESULT 7
 A60957
 thymocyte growth peptide - sheep
 N:Contains: FTS (facteur thymique serique)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: A60957
 R:Ernstroem, U.; Gafvelin, G.; Rudja, J.M.
 Biosci. Rep. 10, 403-412, 1990
 A:Title: Purification of thymocyte growth peptide (TGP) from sheep thymus. Relationship
 A:Reference number: A60957; MUID:91064427; PMID:2249004
 A:Accession: A60957
 A:Molecule type: protein
 A:Residues: 1-9 <ERN>
 A:Cross-references: UNIPROT:Q7M3C5
 A:Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral
 in a variety of immunoassays.
 C:Comment: This peptide was isolated in two forms. One form contained the pyrrolidone car
 x form (thymocyte growth peptide) contains a large, non-peptide blocking group with a hig
 C:Superfamily: thymic factor
 C:Keywords: blocked amino end; pyrrolidone carboxylic acid (Glx) (in FTS) #status experimental
 F:1/Modified site: pyrrolidone carboxylic acid (Glx) (in thymocyte growth peptide) #status experim
 F:1/Modified site: blocked amino end (Glx) (in thymocyte growth peptide) #status experim

 Query Match 29.5%; Score 18; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 1 RMQGG 5
 : |||
 Db 3 KSQGG 7

Query Match 27.9%; Score 17; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels

RESIST 13

Best Local Similarity	75.0%;	Pred. No. 2.8e+05;
Matches	3; Conservative	Indels 0; Gaps 0;
Mismatches	0; Mismatches	1; Indels 0; Gaps 0;

sperm-activating peptide (Thr-5 speract) - sea urchin (Anthocidaris crassispina)
 C:Species: Anthocidaris crassispina
 C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 16-Aug-2004
 C:Accession: H60787
 R:Suzuki, N.; Kajiwara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.
 Comp. Biochem. Physiol. B 89, 687-693, 1988
 A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus
 A:Reference number: A60787; PMID:88242184; PMID:3378407
 A:Accession: H60787
 A:Molecule type: protein
 A:Residues: 1-10 <SUZ>
 A:Cross-references: UNIPROT:Q7M4D6
 C:Comment: This oligopeptide from egg jelly is one of several from this species, all of
 at shows some, but not absolute, species restriction.

Query Match 27.9%; Score 17; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCG 7
 |||
 Db 7 GGVG 10

RESULT 14

F60787
 sperm-activating peptide (Ser-5 speract) - sea urchin (Anthocidaris crassispina)
 C:Species: Anthocidaris crassispina
 C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 16-Aug-2004
 C:Accession: F60787
 R:Suzuki, N.; Kajiwara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.
 Comp. Biochem. Physiol. B 89, 687-693, 1988
 A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus
 A:Reference number: A60787; PMID:88242184; PMID:3378407
 A:Accession: F60787
 A:Molecule type: protein
 A:Residues: 1-10 <SUZ>
 A:Cross-references: UNIPROT:Q7M4D7
 C:Comment: This oligopeptide from egg jelly is one of several from this species, all of
 at shows some, but not absolute, species restriction.

Query Match 27.9%; Score 17; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCG 7
 |||
 Db 7 GGVG 10

RESULT 15

A60787
 sperm-activating peptide (speract) - sea urchin (Hemicentrotus pulcherrimus)
 C:Species: Hemicentrotus pulcherrimus
 C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004
 C:Accession: A60787
 R:Suzuki, N.; Kajiwara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.
 Comp. Biochem. Physiol. B 89, 687-693, 1988
 A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus
 A:Reference number: A60787; PMID:88242184; PMID:3378407
 A:Accession: A60787
 A:Molecule type: protein
 A:Residues: 1-10 <SUZ>
 A:Cross-references: UNIPROT:Q25121
 C:Comment: This oligopeptide from egg jelly is one of several from this species, all of
 at shows some, but not absolute, species restriction.
 C:Superfamily: unassigned animal peptides

Query Match 27.9%; Score 17; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCG 7

Db |||
 7 GGVG 10

Search completed: May 19, 2005, 17:59:33
 Job time : 16 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2005, 17:54:20 ; Search time 111 Seconds
(without alignments)
46.133 Million cell updates/sec

Title: US-09-867-159a-3
Perfect score: 61
Sequence: 1 RMGGGSGSN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 2548

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	29	47.5	10	2 Q6X2S9	Q6X2S9 homo sapien
2	28	45.9	10	2 Q8WP04	Q8WP04 ateles belz
3	26	42.6	9	2 O12096	O12096 caprine art
4	26	42.6	9	2 O12098	O12098 caprine art
5	26	42.6	9	2 O12100	O12100 caprine art
6	26	42.6	9	2 O12102	O12102 caprine art
7	26	42.6	9	2 O12104	O12104 caprine art
8	21	34.4	10	2 P82938	P82938 hordeum vul
9	20	32.8	10	2 Q9X3M2	Q9X3M2 prochloroco
10	19	31.1	9	2 Q92009	Q92009 gallus gall
11	19	31.1	10	2 Q7M501	Q7M501 aspergillus
12	19	31.1	10	2 Q8NEY9	Q8NEY9 homo sapien
13	19	31.1	10	2 Q96QA7	Q96QA7 homo sapien
14	19	31.1	10	2 Q61807	Q61807 mus musculu
15	19	31.1	10	2 Q8UVM2	Q8UVM2 oreochromis
16	18	29.5	8	2 Q15890	Q15890 homo sapien
17	18	29.5	9	1 THVF PIG	P01255 sus scrofa
18	18	29.5	9	2 Q9H373	Q9H373 homo sapien
19	18	29.5	9	2 Q7M3C5	Q7M3C5 ovis aries
20	18	29.5	9	2 Q99JF4	Q99JF4 mus musculu
21	18	29.5	10	2 Q7M0W1	Q7M0W1 streptococc
22	18	29.5	10	2 Q64G36	Q64G36 avian infec
23	17	27.9	7	1 ASCL ALLAS	P84071 allium asca
24	17	27.9	8	2 Q9Y4X6	Q9Y4X6 homo sapien
25	17	27.9	10	2 Q71VB8	Q71VB8 homo sapien
26	17	27.9	10	2 Q7M3T4	Q7M3T4 tripneustes
27	17	27.9	10	2 Q7M3T5	Q7M3T5 tripneustes
28	17	27.9	10	2 Q7M3T6	Q7M3T6 tripneustes
29	17	27.9	10	2 Q7M3T7	Q7M3T7 tripneustes
30	17	27.9	10	2 Q7M3T8	Q7M3T8 tripneustes
31	17	27.9	10	2 Q7M3T9	Q7M3T9 tripneustes

32 17 27.9 10 2 Q7M3U0 tripneustes
33 17 27.9 10 2 Q7M4B2 stronglyloce
34 17 27.9 10 2 Q7M4B3 stronglyloce
35 17 27.9 10 2 Q7M4B4 stronglyloce
36 17 27.9 10 2 Q7M4B5 stronglyloce
37 17 27.9 10 2 Q7M4B6 stronglyloce
38 17 27.9 10 2 Q7M4B9 heterocentr
39 17 27.9 10 2 Q7M4C0 heterocentr
40 17 27.9 10 2 Q7M4C3 echinometra
41 17 27.9 10 2 Q7M4C4 echinometra
42 17 27.9 10 2 Q7M4C5 echinometra
43 17 27.9 10 2 Q7M4C8 stronglyloce
44 17 27.9 10 2 Q7M4D1 hemiceutrot
45 17 27.9 10 2 Q7M4D2 pseudocentr

ALIGNMENTS

RESULT 1
Q6X2S9 PRELIMINARY; PRT; 10 AA.
AC Q6X2S9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Translocase of the inner mitochondrial membrane (Fragment).
GN Name=TIM23;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin.
RX MEDLINE=22890074; PubMed=14527731; DOI=10.1016/S0378-1119(03)00738-8;
RA Meyer R.G., Meyer-Picca M.L., Jacobson E.L., Jacobson M.K.;
RT "Human poly(ADP-ribose) glycohydrolase (PARG) gene and the common
RT promoter sequence it shares with inner mitochondrial membrane
RT translocase 23 (TIM23).";
RL Gene 314,181-190(2003).
DR ENBL; AY258588; AAP83315.1; -
FT NON_TER 10
SQ SEQUENCE 10 AA; 893 MW; 2D7A7165B87878 CRC64;
Query Match 47.5%; Score 29; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 MQGGGSGSN 10
|:|:|:|
DB 1 MEGGGGSGSN 9
RESULT 2
Q8WP04 PRELIMINARY; PRT; 10 AA.
AC Q8WP04;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Oculocutaneous albinism type II (Fragment).
GN Name=OCA2;
OS Ateles belzebuth chamek (Chamek spider monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles.
OX NCBI_TaxID=118643;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21636947; PubMed=11778696; DOI=10.1023/A:1012900206671;
RA Seanez H.N., Lima C.R., Lemos B., Bonvicino C.R., Moreira M.A.M.,
RA Canavez F.C.;
RT "Gene assignment in Ateles paniscus chamek (Platyrrhini, Primates).

RT Allocation of 18 markers of human syntenic groups 1,2,7,14,15,17 and 22.;

RL Chromosome Res. 9:631-639(2001).

DR EMBL; AF375652; AAL31489.1; -.

FT NON_TER 1

SQ SEQUENCE 10 AA; 901 MW; 22DF477DD87EA5B8 CRC64;

Query Match 45.9%; Score 28; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 8.3e+02; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0;

QY 6 CGSC 9

DB 2 CGSC 5

RESULT 3

OL2096 ID OL2096 PRELIMINARY; PRT; 9 AA.

AC OL2096; (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Tat protein (Fragment).

GN Name=at;

OS Caprine arthritis encephalitis virus (CAEV).

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI_TaxID=11660;

RN [1]

RP SEQUENCE FROM N.A.

RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U81439; AAB60832.1; -.

FT NON_TER 1

SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EB8 CRC64;

Query Match 42.6%; Score 26; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.6e+06;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGSC 10

DB 2 GCRLCN 7

RESULT 4

OL2098 ID OL2098 PRELIMINARY; PRT; 9 AA.

AC OL2098; (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Tat protein (Fragment).

GN Name=at;

OS Caprine arthritis encephalitis virus (CAEV).

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI_TaxID=11660;

RN [1]

RP SEQUENCE FROM N.A.

RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U81440; AAB60835.1; -.

FT NON_TER 1

SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EB8 CRC64;

Query Match 42.6%; Score 26; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.6e+06;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGSC 10

DB 2 GCRLCN 7

RESULT 5

OL2100 ID OL2100 PRELIMINARY; PRT; 9 AA.

AC OL2100; (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Tat protein (Fragment).

GN Name=at;

OS Caprine arthritis encephalitis virus (CAEV).

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI_TaxID=11660;

RN [1]

RP SEQUENCE FROM N.A.

RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U81441; AAB60836.1; -.

FT NON_TER 1

SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EB8 CRC64;

Query Match 42.6%; Score 26; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.6e+06;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGSC 10

DB 2 GCRLCN 7

RESULT 6

OL2102 ID OL2102 PRELIMINARY; PRT; 9 AA.

AC OL2102; (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Tat protein (Fragment).

GN Name=at;

OS Caprine arthritis encephalitis virus (CAEV).

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI_TaxID=11660;

RN [1]

RP SEQUENCE FROM N.A.

RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U81442; AAB60838.1; -.

FT NON_TER 1

SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EB8 CRC64;

Query Match 42.6%; Score 26; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.6e+06;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGSC 10

DB 2 GCRLCN 7

RESULT 7

OL2104 ID OL2104 PRELIMINARY; PRT; 9 AA.

AC OL2104; (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Tat protein (Fragment).

GN Name=at;

OS Caprine arthritis encephalitis virus (CAEV).

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI_TaxID=11660;

RN [1]

RP SEQUENCE FROM N.A.

```

RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81443; AAB60840.1; -.
FT NON TER 1
SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EB8 CRC64;

Query Match 42.6%; Score 26; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCGSCN 10
DB 2 GCRCLN 7

RESULT 8
P82938 ID P82938 PRELIMINARY; PRT; 10 AA.
AC P82938
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Unknown endosperm protein C (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. BOMI; TISSUE=Starchy endosperm;
RX MEDLINE=21088911; PubMed=11271488;
RX DOI=10.1002/1522-2683(200011)21:17<3693::AID-ELPS3693>3.0.CO;2-I;
RA Kristoffersen H.E., Flengruid R.;
RT "Separation and characterization of basic barley seed proteins.";
RL Electrophoresis 21:3693-3700(2000)
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
FT NON TER 10
CC PROTEIN IS: 8.5-9.0, ITS MW IS: 11.9 KDA.
FT NON TER 10
SQ SEQUENCE 10 AA; 1053 MW; 9E562DC40AA87AAE CRC64;

Query Match 34.4%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGC 6
DB 1 GGC 3

RESULT 9
Q9X3M2 ID Q9X3M2 PRELIMINARY; PRT; 10 AA.
AC Q9X3M2
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Cytochrome b (Fragment).
GN Names:petB;
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070219; AAD23269.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1076 MW; 75CA5CB05866D324 CRC64;

Query Match 32.8%; Score 20; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.4e+04;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RMOGGCGS 8
DB 3 RKQGISGS 10

RESULT 10
Q92009 ID Q92009 PRELIMINARY; PRT; 9 AA.
AC Q92009
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE C-rel protein (p68-c-rel) (Fragment).
GN Names=c-rel proto-oncogene;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91133738; PubMed=2284104;
RA Hannink M., Temin H.M.;
RT "Structure and autoregulation of the c-rel promoter.";
RL Oncogene 5:1843-1850(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA Hannink M., Temin H.M.;
RT "Structure and auto regulation of the c-rel promoter.";
RL Oncogene 0:0-0(1990).
DR EMBL; X56440; CAA39822.1; -.
DR EMBL; X56515; CAA39866.1; -.
DR PIR; I50633; I50633. 9
FT NON TER 9
SQ SEQUENCE 9 AA; 805 MW; DE317DD87865A2CD CRC64;

Query Match 31.1%; Score 19; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 MQGGCG 7
DB 3 VSGGAG 8

RESULT 11
Q7M501 ID Q7M501 PRELIMINARY; PRT; 10 AA.
AC Q7M501
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polygalacturonase (EC 3.2.1.15) IV (Fragment).
OS Aspergillus sp.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5065;
RN [1]
RP SEQUENCE.
RX MEDLINE=93151962; PubMed=8427629;
RA Stratilova E., Markovic O., Skrovinova D., Rexova-Benkova L.,
RA Jorvall H.;
RT "Pectinase Aspergillus sp. polygalacturonase: multiplicity,
RT divergence, and structural patterns linking fungal, bacterial, and
RT plant polygalacturonases.";
RL J. Protein Chem. 12:15-22(1993).
DR PIR; D61440; D61440.
DR GO; GO:0004650; F:polygalacturonase activity; IEA.
FT NON TER 1

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FT NON TER      10      10
SQ SEQUENCE 10 AA; 959 MW; 845236CSA1A9D1AE CRC64;

Query Match
Best Local Similarity 31.1%; Score 19; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GSC 9
      |||
Db      1 GSC 3

RESULT 12
ID Q8NEY9 PRELIMINARY; PRT; 10 AA.
AC Q8NEY9;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Type II hair-specific keratin (Type II hair keratin) (Fragment).
GN Name=KRTHB6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bairwa N.K., Bamezai R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Bairwa N.K., Bamezai R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037552; AAK68688.1; -.
DR EMBL; AY203963; AAO63472.1; -.
DR GO; GO:0005882; C:intermediate filament; IEA.
KW Keratin.
FT NON TER      10      10
SQ SEQUENCE 10 AA; 1034 MW; 9B53417EAB45B87E CRC64;

Query Match
Best Local Similarity 31.1%; Score 19; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 CGS 8
      |||
Db      3 CGS 5

RESULT 13
ID Q96QA7 PRELIMINARY; PRT; 10 AA.
AC Q96QA7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BA15A2.1 (Cdcs4 guanine exchange factor (GEF) 9 (Collybistin, PEM-2,
DE HPBM-2, KIAA0424) (Fragment).
GN Name=ARHGEF9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Whitehead S.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL451106; CAC88408.1; -.
FT NON TER      10      10
SQ SEQUENCE 10 AA; 1122 MW; 39925CEB878640043 CRC64;

Query Match
Best Local Similarity 31.1%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 CGS 8
      |||
Db      3 CGS 5

us-09-867-159a-3.closed.rup
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 MOGGCG 7
      :|||
Db      4 IRGGSG 9

RESULT 14
ID Q61807 PRELIMINARY; PRT; 10 AA.
AC Q61807;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE LRH-1 protein.
GN Name=Nr5a2; Synonyms=LRH-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alpk:APFCD-1; TISSUE=Liver;
RX MEDLINE=22755858; PubMed=12672674;
RA Liu D.L., Liu W.Z., Li Q.L., Wang H.M., Qian D., Treuter E., Zhu C.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M81385; AAA39446.1; -.
DR PIR; S27873; S27873.
DR MGD; MGI:1346834; Nr5a2.
DR GO; GO:0003677; F:DNA binding; IDA.
DR GO; GO:0008206; P:bile acid metabolism; IMP.
DR GO; GO:0042632; P:cholesterol homeostasis; IMP.
SQ SEQUENCE 10 AA; 1133 MW; 998B68F5B7244EA5 CRC64;

Query Match
Best Local Similarity 31.1%; Score 19; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 SCN 10
      |||
Db      3 SCN 5

RESULT 15
ID Q8UWV2 PRELIMINARY; PRT; 10 AA.
AC Q8UWV2;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE AMPA receptor subunit 2 alpha (Fragment).
GN Name=Glur2a;
OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8127;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21617183; PubMed=11741603; DOI=10.1016/S0014-5793(01)03183-0;
RA Kung S.-S., Chen Y.-C., Lin W.-H., Chen C.-C., Chow W.-Y.;
RT "Q/R RNA editing of the AMPA receptor subunit 2 (GRIA2) transcript
RT involves no later than the appearance of cartilaginous fishes.";
DR FEBS Lett. 509:277-281(2001).
DR EMBL; AF350050; AAL57192.1; -.

```

DR GO:0004872; F:receptor activity; IEA.

KW Receptor.

FT NON_TER 1

1

FT NON_TER 10

10

SQ SEQUENCE 10 AA; 1153 MW; 721A6ESAEB866C4 CRC64;

Query Match: 31.1%; Score 19; DB 2; Length 10;

Best Local Similarity 60.0%; Pred. No. 2e+04;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 MQGQC 6

1: 11

Db 2 MRQGC 6

Search completed: May 19, 2005, 18:15:42

Job time : 114 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:47:19 ; Search time 141 Seconds
(without alignments)
27.430 Million cell updates/sec

Title: US-09-867-159A-3

Perfect score: 61

Sequence: 1 RMQGGCGSCN 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 465227

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	10	5 AAO20569	Cysteine
2	61	100.0	10	5 ABB51909	Cysteine
3	37	60.7	8	2 AAR77350	Cysteine
4	36	59.0	9	2 ADI11045	Somatosta
5	36	59.0	9	2 ADI11044	Somatosta
6	36	59.0	9	6 ABUS5751	Polylinke
7	36	59.0	9	2 ADF69793	M. tuberc
8	36	59.0	10	2 ADI11047	Somatosta
9	32	52.5	10	4 AAG86614	Saccharom
10	31	50.8	8	2 AAW41566	Human cal
11	31	50.8	8	4 AAB97506	Peptide n
12	30	49.2	6	5 ABB08544	Human HCC
13	30	49.2	6	6 ABUS5750	Polylinke
14	30	49.2	6	7 ADF69792	M. tuberc
15	30	49.2	8	4 AAB97503	Peptide n
16	30	49.2	10	2 AAR69298	Gp IIB/II
17	30	49.2	10	2 ADD67499	Specific-
18	30	49.2	10	2 AAW60340	Tumour ho
19	30	49.2	10	2 AAW50579	GPIIb/III
20	30	49.2	10	2 AAW93666	Human bre
21	30	49.2	10	2 ADE25476	TC-99m la
22	30	49.2	10	3 AAY54962	Peptide 1
23	30	49.2	10	3 AAY95503	GPIIb/III
24	30	49.2	10	3 AAB21757	Human bre
25	30	49.2	10	4 AAE06335	Human bre

26	30	49.2	10	5 ABB51909	Abb51909 Human 34P
27	30	49.2	10	5 ABB51815	Abb51815 Human 34P
28	30	49.2	10	5 ABB51593	Abb51593 Human 34P
29	30	49.2	10	5 ABB51491	Abb51491 Human 34P
30	30	49.2	10	5 ABB51705	Abb51705 Human 34P
31	29	47.5	8	2 AAW52097	AAW52097 Targettin
32	29	47.5	8	2 AAY27435	AAY27435 Rat HICP
33	29	47.5	8	5 AAO20971	AAO20971 8-mer ins
34	29	47.5	8	5 AAB15661	AAB15661 Insulin-1
35	29	47.5	8	6 ABP56100	ABP56100 Human IGF
36	29	47.5	8	7 ADH02887	ADH02887 AscII pep
37	29	47.5	8	7 ADH02888	ADH02888 Sali pep
38	29	47.5	9	2 AAW06390	AAW06390 Cyclic pe
39	29	47.5	9	2 ADE25470	ADE25470 GPIIb/III
40	29	47.5	9	2 ADE25444	ADE25444 GPIIb/III
41	29	47.5	9	2 ADH59029	ADH59029 GFIIb/IIa
42	29	47.5	9	3 AAY54928	AAY54928 Peptide 1
43	29	47.5	9	4 AAG88625	AAG88625 HER2/NEU
44	29	47.5	9	8 ADE64416	ADE64416 Radiophar
45	29	47.5	9	8 ADH58651	ADH58651 Radiophar

ALIGNMENTS

RESULT 1
AAO20569
ID AAO20569 standard; peptide; 10 AA.
XX AC AAO20569;
XX DT 02-JAN-2003 (first entry)
XX DE Cysteine protease. epitope peptide region, SEQ ID No 3.
XX KW Antiallergic; antiinflammatory; antiasthmatic; dermatological; allergen;
XX KW anti-histamine; histamine synthesis inhibitor; allergic hypersensitivity;
XX KW allergic asthma; allergic rhinitis; cysteine protease protein; enzyme;
XX KW atopic eczema; epitope.
XX OS Dermatophagoides pteronyssinus.
XX PN WO200278736-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-FR001098.
XX PR 30-MAR-2001; 2001FR-00004370.
XX PR 03-MAY-2001; 2001FR-00005929.
XX PR 29-MAY-2001; 2001US-00867159.
XX PA (ANTI-) ANTIALIS SARKL.
XX PI Loria E, Terrasse G, Trehin Y;
XX WPI; 2002-750636/81.
XX DR Antiallergic compositions containing an anti-histamine, a histamine
XX PT synthesis inhibitor, and optionally an allergen or nucleic acid coding
XX PT for the allergen.
XX PS Claim 14; Page 11; 32pp; French.
XX CC The invention relates to antiallergic compositions containing an anti-
XX CC histamine, a histamine synthesis inhibitor, and optionally an allergen or
XX CC isolated nucleic acid molecule that has at least one polynucleotide
XX CC sequence coding for the allergen, together with a pharmaceutical carrier.
XX CC The pharmaceutical composition of the invention is useful as a non-
XX CC specific antiallergic treatment, and also useful in the treatment of
XX CC allergic hypersensitivity, allergic asthma, allergic rhinitis, and
XX CC allergic and atopic eczema. This sequence represents a peptide of a
XX CC cysteine protease epitope region relating to the antiallergic

CC compositions of the invention
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 61; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 0.027;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMGGCGGSCN 10
 |||||
 Db 1 RMGGCGGSCN 10

RESULT 2

ABB98534
 ID ABB98534 standard; peptide; 10 AA.

XX AC ABB98534;

XX DT 13-DEC-2002 (first entry)

XX DE Cysteine protease epitope #1.

XX KW Antiallergic; antiasthmatic; antiinflammatory; dermatological;
 KW immunotherapy; allergen; allergic hypersensitivity reaction;
 KW allergic asthma; allergic rhinitis; allergic atopic eczema;
 KW cysteine protease.

XX OS Dermatophagoides pteronyssinus.

XX PN FR2822709-A1.

XX PD 04-OCT-2002.

XX PF 03-MAY-2001; 2001FR-00005929.

XX PR 30-MAR-2001; 2001FR-00004370.

XX PA (ANTI-) ANTIALIS SARL.

XX PI Loria E, Terrasse G, Trehin Y;

XX WPI; 2002-735037/80.

XX PT Antiallergic composition, useful for preventing and treating e.g. asthma,
 PT rhinitis or eczema, containing at least two of allergen, antihistamine
 PT and histamine synthesis inhibitor.

XX PS Claim 8; Page 6; 33pp; French.

XX CC The present invention relates to an antiallergic pharmaceutical
 CC composition (I) comprising a pharmaceutical carrier containing an active
 CC agent combination of at least two of: an allergen; an antihistamine; and
 CC a histamine synthesis inhibitor. (I) is used for treating or preventing
 CC allergic hypersensitivity reactions, especially allergic asthma, allergic
 CC rhinitis or allergic atopic eczema, in babies, children or adults. The
 CC present sequence is a peptide fragment (epitope) of cysteine protease
 CC from Dermatophagoides pteronyssinus, which was used as an allergen in the
 CC invention

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 61; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 0.027;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMGGCGGSCN 10
 |||||
 Db 1 RMGGCGGSCN 10

RESULT 3

AAR77350

ID AAR77350 standard; peptide; 8 AA.

XX AC AAR77350;

XX DT 14-MAY-1996 (first entry)

XX DE Cysteine proteinase derived peptide #1.

XX KW Primer; amplify; polymerase chain reaction; PCR; Haemonchus contortus;
 KW cysteine proteinase; DM.2; DM.3; DM.4; human; DM.4a; DM.5; antigen;
 KW vaccine; helminth; parasite; DM.1; ruminant; gastro-intestinal tract.

XX OS Haemonchus contortus.

XX PN WO9526402-A1.

XX PD 05-OCT-1995.

XX PF 24-MAR-1995; 95WO-GB000665.

XX PR 25-MAR-1994; 94GB-00005925.

XX PR 25-MAR-1994; 94GB-00005990.

XX PA (MLCW) MALLINCKRODT VETERINARY INC.

XX PI Knox DP, Smith SK, Smith WD, Redmond D, Murray J;

XX WPI; 1995-351322/45.

XX DR N-PSDB; AAQ94240.

XX PT Protective helminth parasite antigen - used in vaccine directed against
 PT parasitic nematodes of mammalian gastro-intestinal tract e.g. Haemonchus
 PT contortus.

XX PS Example 16; Fig 15; 79pp; English.

XX CC The sequences given in AAR77350-53 are peptides derived from the
 CC canonical Haemonchus contortus cysteine proteinase molecule which were
 CC used in the design of the primers given in AAQ94240-43. These primers
 CC were used in the cloning of cDNA fragments from the cysteine proteinase
 CC gene, such as DM.1, DM.2, DM.3, DM.4, DM.4a and DM.5 (see also AAQ94246-
 CC 51). The amplified fragments may be expressed in a recombinant cell for
 CC the production of antigens. These antigens may be used in the preparation
 CC of a vaccine against helminth parasites in a human or non-human animal

XX SQ Sequence 8 AA;

Query Match 60.7%; Score 37; DB 2; Length 8;

Best Local Similarity 85.7%; Pred. No. 1.8e+06;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 QGCGGSC 9

Db 1 QGCGGSC 7

RESULT 4

AD111045

ID AD111045 standard; peptide; 9 AA.

XX AC AD111045;

XX DT 15-APR-2004 (first entry)

XX DE Somatostatin analogue peptide SEQ ID NO:60.

XX KW dihydropyridine/pyridinium salt type redox moiety; retina; lipophilic;
 KW antidiabetic; ophthalmological; diabetic retinopathy;
 KW growth factor inhibitory activity; somatostatin; somatostatin analogue;
 KW octreotide; lanreotide; sequential metabolism;
 KW insulin dependent diabetes mellitus.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Xaa = Nic"
 FT Disulfide-bond 4. .7
 FT Modified-site 9
 FT /note= "Xaa = OH"
 XX WO9912572-A1.
 PN 18-MAR-1999.
 XX PD
 XX PF 01-SEP-1998; 98WO-US017987.
 XX PR 10-SEP-1997; 97US-0058423P.
 XX PA (UYFL) UNIV FLORIDA.
 XX PI Bodor NS, Grant MB;
 XX WPI; 1999-263364/22.
 XX New peptide derivatives with redox targetor moiety are useful in the treatment of diabetic retinopathy.
 XX Example 6; SEQ ID NO 60; 186pp; English.
 XX The present invention describes peptide derivatives (I) comprising a dihydropyridine/pyridinium salt type redox moiety for targeting peptides to the retina, a bulky lipophilic function and an amino acid/dipeptide/tripeptide spacer. Also described: (1) the preparation of (I); and (2) intermediate quaternary salts (II). (I) have antidiabetic and ophthalmological activities. (I) can be used in the treatment or prevention of diabetic retinopathy by delivery of peptides with growth factor inhibitory activity (e.g. somatostatin analogues such as octreotide and lanreotide) to the retina by sequential metabolism. It is envisaged that (I) will be useful in the treatment of insulin dependent diabetes mellitus patients for critical periods in diabetic retinopathy disease progression before laser photocoagulation is indicated, preferably for 1-4 month intervals when a patient is experiencing severe non-proliferative diabetic retinopathy or is found to have low risk diabetic retinopathy. The present sequence represents a somatostatin analogue peptide, which is used in the exemplification of the present invention.
 XX SQ Sequence 9 AA;

Query Match 59.0%; Score 36; DB 2; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCGGSC 9
 |||||
 Db 2 GCGGSC 7

RESULT 5
 ADI11044
 ID ADI11044 standard; peptide; 9 AA.
 XX AC ADI11044;
 XX 15-APR-2004 (first entry)

XX Somatostatin analogue peptide SEQ ID NO:59.
 XX dihydropyridine/pyridinium salt type redox moiety; retina; lipophilic; KW antidiabetic; ophthalmological; diabetic retinopathy;
 KW growth factor inhibitory activity; somatostatin; somatostatin analogue;
 KW octreotide; lanreotide; sequential metabolism;
 KW insulin dependent diabetes mellitus.
 XX Synthetic.
 OS

XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Xaa = Trig"
 FT Disulfide-bond 4. .7
 FT Modified-site 9
 FT /note= "Xaa = OH"
 XX WO9912572-A1.
 PN 18-MAR-1999.
 XX PD
 XX PF 01-SEP-1998; 98WO-US017987.
 XX PR 10-SEP-1997; 97US-0058423P.
 XX PA (UYFL) UNIV FLORIDA.
 XX PI Bodor NS, Grant MB;
 XX WPI; 1999-263364/22.
 XX New peptide derivatives with redox targetor moiety are useful in the treatment of diabetic retinopathy.
 XX Example 6; SEQ ID NO 59; 186pp; English.
 XX The present invention describes peptide derivatives (I) comprising a dihydropyridine/pyridinium salt type redox moiety for targeting peptides to the retina, a bulky lipophilic function and an amino acid/dipeptide/tripeptide spacer. Also described: (1) the preparation of (I); and (2) intermediate quaternary salts (II). (I) have antidiabetic and ophthalmological activities. (I) can be used in the treatment or prevention of diabetic retinopathy by delivery of peptides with growth factor inhibitory activity (e.g. somatostatin analogues such as octreotide and lanreotide) to the retina by sequential metabolism. It is envisaged that (I) will be useful in the treatment of insulin dependent diabetes mellitus patients for critical periods in diabetic retinopathy disease progression before laser photocoagulation is indicated, preferably for 1-4 month intervals when a patient is experiencing severe non-proliferative diabetic retinopathy or is found to have low risk diabetic retinopathy. The present sequence represents a somatostatin analogue peptide, which is used in the exemplification of the present invention.
 XX SQ Sequence 9 AA;

Query Match 59.0%; Score 36; DB 2; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCGGSC 9
 |||||
 Db 2 GCGGSC 7

RESULT 6
 ABUS5751
 ID ABUS5751 standard; peptide; 9 AA.
 XX AC ABUS5751;
 XX 18-MAR-2003 (first entry)

XX Polylinker peptide #3 relating to invention of M. tuberculosis antigens.
 XX Mycobacterium tuberculosis antigenic polypeptide; immune response; KW tuberculosis infection; polylinker peptide.
 XX Synthetic.
 OS
 PN US6465633-B1.
 XX

```

PD 15-OCT-2002.
XX
XX 23-DEC-1999; 99US-00470191.
XX
XX 24-DEC-1998; 98US-0113952P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky Y;
XX
XX WPI; 2003-147072/14.
XX
XX Novel isolated mycobacterial polynucleotide, useful for treating,
XX preventing or diagnosing Mycobacterium tuberculosis infection, for
XX producing Mycobacterium tuberculosis secretory polypeptides and DNA
XX vaccines.
XX
XX Disclosure; Col 89; 48pp; English.
XX
XX The present invention relates to the isolation of polynucleotide
XX sequences encoding Mycobacterium tuberculosis antigenic polypeptides. The
XX polynucleotide sequences of the invention are useful for treating,
XX preventing, and diagnosing M. tuberculosis infection, for producing M.
XX tuberculosis secretory polypeptides, for producing DNA vaccines, for
XX diagnostic purposes, as molecular probes or primers to detect the
XX presence of bacteria in a biological sample, for inducing and/or
XX enhancing immune responses to M. tuberculosis, and in gene therapy.
XX ABUS5749-ABUS5754 represent flexible polylinker peptides. Note: The
XX present sequence is given in the Sequence listing but is not mentioned
XX elsewhere in the specification
XX
XX Sequence 9 AA;
XX
Query Match 59.0%; Score 36; DB 6; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 GCGGSC 9
DB 3 GCGGCG 8
RESULT 7
ADF69793
ID ADF69793 standard; peptide; 9 AA.
XX
XX ADF69793;
XX
XX 12-FEB-2004 (first entry)
XX
XX M. tuberculosis fusion protein associated flexible polylinker peptide #2.
XX
XX Fusion protein; Mycobacterium tuberculosis antigen;
XX tuberculosis infection; immune response; tuberculostatic;
XX flexible polylinker.
XX
XX Synthetic.
XX
XX US2003147911-A1.
XX
XX 07-AUG-2003.
XX
XX 05-FEB-2003; 2003US-00359460.
XX
XX 13-MAR-1997; 97US-00818112.
XX
XX 01-OCT-1997; 97US-00942578.
XX
XX 18-FEB-1998; 98US-00025197.
XX
XX 07-APR-1998; 98US-00056556.
XX
XX 30-DEC-1998; 98US-00223040.
XX
XX 07-APR-1999; 99US-00287849.
XX
XX (CORI-) CORIXA CORP.
XX
PI Reed SG, Skeiky YA, Dillon DC, Alderson M, Campos-Neto A;
XX
XX WPI; 2003-897524/82.
XX
XX New fusion proteins of Mycobacterium tuberculosis for diagnosing,
XX preventing or treating tuberculosis infection or in enhancing immune
XX responses in M. tuberculosis.
XX
XX Disclosure; SEQ ID NO 43; 135pp; English.
XX
XX The present invention relates to fusion proteins of Mycobacterium
XX tuberculosis antigens, and the polynucleotide sequences encoding them.
XX The sequences of the invention are useful in a method for preventing
XX tuberculosis by administering to a subject an amount of the fusion
XX protein or the polynucleotide that encodes the fusion protein. Also
XX disclosed is a pharmaceutical composition comprising the fusion protein
XX or the polynucleotide sequence encoding it. The fusion protein induces an
XX immune response to M. tuberculosis and can be used in the diagnosis,
XX prevention, and treatment of tuberculosis infection. The present sequence
XX represents a flexible polylinker peptide.
XX
XX Sequence 9 AA;
XX
Query Match 59.0%; Score 36; DB 7; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 GCGGSC 9
DB 3 GCGGCG 8
RESULT 8
AD111047
ID AD111047 standard; peptide; 10 AA.
XX
XX AD111047;
XX
XX 15-APR-2004 (first entry)
XX
XX Somatostatin analogue peptide SEQ ID NO:62.
XX
XX dihydropyridine/pyridinium salt type redox moiety; retina; lipophilic;
XX antidiabetic; ophthalmological; diabetic retinopathy;
XX growth factor inhibitory activity; somatostatin; somatostatin analogue;
XX octreotide; lanreotide; sequential metabolism;
XX insulin dependent diabetes mellitus.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1 /note= "Xaa = TFA"
XX Modified-site 2 /note= "Xaa = Nic"
XX Disulfide-bond 5..8
XX Modified-site 10 /note= "Xaa = OH"
XX
XX WO9912572-A1.
XX
XX 18-MAR-1999.
XX
XX 01-SEP-1998; 98WO-US017987.
XX
XX 10-SEP-1997; 97US-0058423P.
XX
XX (UYFL ) UNIV FLORIDA.
XX
XX Bodor NS, Grant MB;
XX
XX WPI; 1999-263364/22.
XX

```

PT New peptide derivatives with redox targetor moiety are useful in the
 PT treatment of diabetic retinopathy.

XX Example 10; SEQ ID NO 62; 186pp; English.

PS The present invention describes peptide derivatives (I) comprising a
 CC dihydropyridine/pyridinium salt type redox moiety for targeting peptides
 CC to the retina, a bulky lipophilic function and an amino
 CC acid/dipeptide/tripeptide spacer. Also described: (I) the preparation of
 CC (1); and (2) intermediate quaternary salts (II). (I) have antidiabetic
 CC and ophthalmological activities. (I) can be used in the treatment or
 CC prevention of diabetic retinopathy by delivery of peptides with growth
 CC factor inhibitory activity (e.g. somatostatin analogues such as
 CC octreotide and lanreotide) to the retina by sequential metabolism. It is
 CC envisaged that (I) will be useful in the treatment of insulin dependent
 CC diabetes mellitus patients for critical periods in diabetic retinopathy
 CC disease progression before laser photocoagulation is indicated.
 CC preferably for 1-4 month intervals when a patient is experiencing severe
 CC non-proliferative diabetic retinopathy or is found to have low risk
 CC diabetic retinopathy. The present sequence represents a somatostatin
 CC analogue peptide, which is used in the exemplification of the present
 CC invention.

XX Sequence 10 AA;

Query Match 59.0%; Score 36; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCGSC 9
 Db 3 GGCGC 8

RESULT 9

AAG86614
 ID AAG86614 standard; peptide; 10 AA.

XX AAG86614;

DT 11-SEP-2001 (first entry)

DE Saccharomyces cerevisiae peptide, SEQ ID NO: 1563.

XX Saccharomyces cerevisiae; complementary peptide; peptide identification;
 KW drug discovery; drug design.

XX Saccharomyces cerevisiae.

XX WO200142276-A1.

PN 14-JUN-2001.

XX 13-DEC-2000; 2000WO-GB004773.

XX 13-DEC-1999; 99GB-00029471.

XX (PROT-) PROTEOM LTD.

XX Roberts GW, Heal JR;

XX WPI; 2001-367863/38.

XX Identifying complementary peptides by analysis of protein and nucleotide
 PT sequence databases, useful in drug design.

PS Example 3; Page 245; 488pp; English.

XX The invention relates to the identification of complementary peptides by
 CC analysis of protein and nucleotide sequence databases from higher
 CC eukaryotic genomes, excluding human and plants. The specific
 CC complementary peptides interact with their relevant target proteins
 CC encoded in the eukaryote genome. The peptides may be used as reagents and

CC drugs for drug discovery and as lead ligands for drug design and
 CC development. The present sequence is a complementary peptide from
 CC Saccharomyces cerevisiae

XX Sequence 10 AA;

Query Match 52.5%; Score 32; DB 4; Length 10;
 Best Local Similarity 71.4%; Pred. No. 4.3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 MOGGCGS 8
 Db 4 VSGGCGS 10

RESULT 10

AAW41566

ID AAW41566 standard; peptide; 8 AA.

XX AAW41566;

DT 27-APR-1998 (first entry)

DE Human calpain partial peptide.

XX Calpain; human; leukocyte; calcium dependent cysteine protease;
 KW screening; activator; inhibitor; treatment; prevention; cancer;
 KW cerebral apoplexy; cerebral infarction; subarachnoid haemorrhage;
 KW Alzheimer's disease; myodystrophy; cataracts; collagen disease;
 KW ischaemic heart disease; atherosclerosis; arthritis.

XX Homo sapiens.

PN EP799892-A2.

XX 08-OCT-1997.

XX 03-APR-1997; 97BP-00105508.

XX 05-APR-1996; 96JP-00083649.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Shintani Y, Nishi K, Kawamoto T;

XX WPI; 1997-482674/45.

XX N-PSDB; AAV04204.

XX Human calpain protein and related DNA - useful for drug screening and
 PT treating cancer, stroke, etc.

XX Disclosure; Page 29; 43pp; English.

XX The present sequence is a calpain partial peptide. Calpain is a human
 CC leukocyte derived calcium dependent cysteine protease, which can be used
 CC to screen for compounds that activate or inhibit its proteolytic
 CC activity. Calpain DNA can be used to treat or prevent cancer, cerebral
 CC apoplexy, cerebral infarction, subarachnoid haemorrhage, Alzheimer's
 CC disease, myodystrophy, cataracts, ischaemic heart disease,
 CC atherosclerosis, arthritis or collagen disease

XX Sequence 8 AA;

Query Match 50.8%; Score 31; DB 2; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 QGGCGSC 9

Db 2 QGGGDC 8

RESULT 11

AAB97506
 ID AAB97506 standard; peptide; 8 AA.
 AC AAB97506;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE Peptide nucleic acid peptide fragment #4.
 DE
 KW Peptide nucleic acid; PNA; therapy; infection; cancer; restenosis;
 KW asthma; autoimmune disorder; endocrinological disorder; renal failure;
 KW neurological disease; acromegaly; sickle cell anaemia;
 KW polyamide backbone.
 XX
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /label= OTHER
 FT /note= "optionally bound to AAH23598"
 FT Misc-difference 5
 FT /label= OTHER
 FT /note= "optionally D-form residue"
 FT
 XX US6180767-B1.
 XX
 XX 30-JAN-2001.
 PD
 XX
 PF 07-JAN-1997; 97US-00779072.
 XX
 PR 11-JAN-1996; 96US-0009747P.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Wickstrom E, Basu S;
 XX
 DR WPI; 2001-342005/36.
 XX
 XX Novel conjugate, useful for killing pathogenic organisms and for
 PT inhibiting gene expression, comprising a peptide nucleic acid oligomer
 PT conjugated to ligand capable of binding to a cell surface receptor via a
 PT chemical bond or linker.
 XX
 PS Example 1; Col 22; 25pp; English.
 CC
 CC The present invention provides a number of peptide nucleic acids (PNAs)
 CC capable of binding to a cell surface receptor, where the oligomer and the
 CC peptide are linked by a chemical bond or an amino acid linker. The
 CC oligomer may have a polyamide, polythioamide, polysulfonamide or
 CC polysulfonamide backbone. The PNAs of the invention can be used in
 CC therapy, including the treatment of infections, cancer, autoimmune
 CC diseases, renal failure, endocrinological disorders, acromegaly,
 CC neurological diseases and sickle cell anaemia. The present sequence is an
 CC example of a peptide for use in a PNA
 XX
 SQ Sequence 8 AA;
 Query Match 50.8%; Score 31; DB 4; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 GCGGSC 9
 DB 3 GGCAC 8
 ||| :
 RESULT 12
 ABB08544
 ID ABB08544 standard; protein; 6 AA.
 XX
 AC ABB08544;
 XX
 DT 23-MAY-2002 (first entry)

XX Human HCCAl PCR primer P4.
 XX
 KW HCCAl; liver cancer; cytostatic; human.
 XX
 OS Homo sapiens.
 XX
 PN CN1322732-A.
 XX
 PD 21-NOV-2001.
 XX
 PF 08-MAY-2000; 2000CN-00115595.
 XX
 PR 08-MAY-2000; 2000CN-00115595.
 XX
 PA (SHAN-) SHANGHAI DONGFANG LIVER & GALLBLADDER SU.
 XX
 PI Wang H, Zeng J, Wu M;
 XX
 DR WPI; 2002-148617/20.
 XX
 PT New liver cancer up expressing gene for treating liver cancer and other
 PT diseases.
 XX
 PS Example 5; Page 16 (disclosure); 31pp; Chinese.
 XX
 CC The present invention discloses new human HCCAl protein, the
 CC polynucleotides encoding the polypeptide and the recombinant process to
 CC produce the polypeptide. The present invention also discloses the method
 CC of applying the medicine composite of the polypeptide in treating liver
 CC cancer and other diseases. The present invention also discloses the
 CC preparation process of HCCAl protein specific antibody and its
 CC application in diagnosing and treating diseases. The present invention
 CC also discloses the application of the polynucleotides encoding the new
 CC HCCAl protein. The present sequence represents a peptide sequence
 CC relating to human HCCAl protein
 XX
 SQ Sequence 6 AA;
 Query Match 49.2%; Score 30; DB 5; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 CGGCN 10
 DB 1 CGGCN 5
 |||
 RESULT 13
 ABUS5750
 ID ABUS5750 standard; peptide; 6 AA.
 XX
 AC ABUS5750;
 XX
 DT 18-MAR-2003 (first entry)
 XX
 DE Polylinker peptide #2 relating to invention of M. tuberculosis antigens.
 KW Mycobacterium tuberculosis antigenic polypeptide; immune response;
 KW tuberculosis infection; polylinker peptide.
 XX
 OS Synthetic.
 XX
 PN US6465633-B1.
 XX
 PD 15-OCT-2002.
 XX
 PF 23-DEC-1999; 99US-00470191.
 XX
 PR 24-DEC-1998; 98US-0113952P.
 XX
 PA (CORI-) CORIXA CORP.
 XX

PI Skeiky Y;
 XX WPI; 2003-147072/14.
 XX
 XX Novel isolated mycobacterial polynucleotide, useful for treating,
 PT preventing or diagnosing Mycobacterium tuberculosis infection, for
 PT producing Mycobacterium tuberculosis secretory polypeptides and DNA
 PT vaccines.
 XX
 XX Disclosure; Col 89; 48pp; English.
 XX
 XX The present invention relates to the isolation of polynucleotide
 CC sequences encoding Mycobacterium tuberculosis antigenic polypeptides. The
 CC polynucleotide sequences of the invention are useful for treating,
 CC preventing, and diagnosing M. tuberculosis infection, for producing M.
 CC tuberculosis secretory polypeptides, for producing DNA vaccines, for
 CC diagnostic purposes, as molecular probes or primers to detect the
 CC presence of bacteria in a biological sample, for inducing and/or
 CC enhancing immune responses to M. tuberculosis, and in gene therapy.
 CC AB055749-AB055754 represent flexible polylinker peptides. Note: The
 CC present sequence is given in the Sequence listing but is not mentioned
 CC elsewhere in the specification
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 49.2%; Score 30; DB 6; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 GCGGC 9
 Db 1 GCGGC 5
 |||||
 RESULT 14
 ADF69792
 ID ADF69792 standard; peptide; 6 AA.
 XX AC ADF69792;
 XX
 XX 12-FEB-2004 (first entry)
 DT
 XX M. tuberculosis fusion protein associated flexible polylinker peptide #1.
 DE
 XX Fusion protein; Mycobacterium tuberculosis antigen;
 KW tuberculosis infection; immune response; tuberculostatic;
 KW flexible polylinker.
 XX
 OS Synthetic.
 XX
 XX US2003147911-A1.
 PN
 XX 07-AUG-2003.
 PD
 XX
 XX 05-FEB-2003; 2003US-00359460.
 PF
 XX 13-MAR-1997; 97US-00818112.
 PR 01-OCT-1997; 97US-00942578.
 PR 18-FEB-1998; 98US-00025197.
 PR 07-APR-1998; 98US-00056556.
 PR 30-DEC-1998; 98US-00223040.
 PR 07-APR-1999; 99US-00287849.
 XX
 XX (CORI-) CORIXA CORP.
 PA
 XX
 XX Reed SG, Skeiky YA, Dillon DC, Alderson M, Campos-Neto A;
 PI WPI; 2003-897524/82.
 XX
 XX New fusion proteins of Mycobacterium tuberculosis for diagnosing,
 PT preventing or treating tuberculosis infection or in enhancing immune
 PT responses in M. tuberculosis.
 XX

PS Disclosure; SEQ ID NO 42; 135pp; English.
 XX
 XX The present invention relates to fusion proteins of Mycobacterium
 CC tuberculosis antigens, and the polynucleotide sequences encoding them.
 CC The sequences of the invention are useful in a method for preventing
 CC tuberculosis by administering to a subject an amount of the fusion
 CC protein or the polynucleotide that encodes the fusion protein. Also
 CC disclosed is a pharmaceutical composition comprising the fusion protein
 CC or the polynucleotide sequence encoding it. The fusion protein induces an
 CC immune response to M. tuberculosis and can be used in the diagnosis,
 CC prevention, and treatment of tuberculosis infection. The present sequence
 CC represents a flexible polylinker peptide.
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 49.2%; Score 30; DB 7; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 GCGSC 9
 Db 1 GCGSC 5
 |||||
 RESULT 15
 AAB97503
 ID AAB97503 standard; peptide; 8 AA.
 XX AC AAB97503;
 XX
 XX 14-AUG-2001 (first entry)
 DT
 XX Peptide nucleic acid peptide fragment #1.
 XX
 XX Peptide nucleic acid; PNA; therapy; infection; cancer; restenosis;
 KW asthma; autoimmune disorder; endocrinological disorder; renal failure;
 KW neurological disease; acromegaly; sickle cell anaemia;
 KW polyamide backbone.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1 /label= OTHER
 FT /note= "optionally bound to AAH23598"
 FT Modified-site 5
 FT /label= OTHER
 FT /note= "optionally 4-methoxybenzyl-Cys, optionally D-form
 FT residue"
 FT Modified-site 6
 FT /label= OTHER
 FT /note= "optionally modified by benzyl, optionally D-form
 FT residue"
 FT Modified-site 7
 FT /label= OTHER
 FT /note= "optionally modified by phenylmethoxycarbonyl,
 FT optionally D-form residue"
 FT Modified-site 8
 FT /label= OTHER
 FT /note= "optionally modified by phenylmethoxycarbonyl and
 FT resin, optionally D-form residue"
 XX
 XX US6180767-B1.
 PN
 XX 30-JAN-2001.
 PD
 XX 07-JAN-1997; 97US-00779072.
 PF
 XX 11-JAN-1996; 96US-0009747P.
 PR
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA
 XX Wickstrom E, Basu S;
 PI

XX WPI; 2001-342005/36.
DR
XX
PT Novel conjugate, useful for killing pathogenic organisms and for
PT inhibiting gene expression, comprising a peptide nucleic acid oligomer
PT conjugated to ligand capable of binding to a cell surface receptor via a
PT chemical bond or linker.
XX
PS Claim 14; Col 19; 25pp; English.
XX
CC The present invention provides a number of peptide nucleic acids (PNAs)
CC capable of binding to a cell surface receptor, where the oligomer and the
CC peptide are linked by a chemical bond or an amino acid linker. The
CC oligomer may have a polyamide, polythioamide, polysulfonamide or
CC polysulfonamide backbone. The PNAs of the invention can be used in
CC therapy, including the treatment of infections, cancer, autoimmune
CC diseases, renal failure, endocrinological disorders, acromegaly,
CC neurological diseases and sickle cell anaemia. The present sequence is an
CC example of a peptide for use in a PNA
XX
SQ Sequence 8 AA;
Query Match 49.2%; Score 30; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY . 4 GGCGSC 9
Db |||||
3 GGCSKC 8
Search completed: May 19, 2005, 17:59:05
Job time : 147 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:59:41 ; Search time 89.5 Seconds
(without alignments)
37.375 Million cell updates/sec

Title: US-09-867-159A-3

Perfect score: 61

Sequence: 1 RMOGGCGSCN 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 185062

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*

17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*

18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*

19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	10	US-09-867-159A-3	Sequence 3, Appl
2	36	59.0	7	US-10-175-833-59	Sequence 59, Appl
3	36	59.0	7	US-10-175-833-60	Sequence 60, Appl
4	36	59.0	7	US-10-175-833-62	Sequence 62, Appl
5	36	59.0	9	US-09-287-849-43	Sequence 43, Appl
6	36	59.0	9	US-10-359-460-43	Sequence 43, Appl
7	36	59.0	9	US-10-359-459-7	Sequence 7, Appl
8	33	54.1	8	US-10-163-415-2	Sequence 2, Appl
9	31.5	51.6	8	US-10-678-961B-62	Sequence 62, Appl
10	31.5	51.6	8	US-10-702-228A-62	Sequence 62, Appl
11	30	49.2	6	US-09-287-849-42	Sequence 42, Appl
12	30	49.2	6	US-10-359-460-42	Sequence 42, Appl
13	30	49.2	6	US-10-359-459-6	Sequence 6, Appl

14	30	49.2	10	9	US-09-765-086-57	Sequence 57, Appl
15	30	49.2	10	9	US-09-779-308-222	Sequence 222, App
16	30	49.2	10	9	US-09-779-308-324	Sequence 324, App
17	30	49.2	10	9	US-09-779-308-436	Sequence 436, App
18	30	49.2	10	9	US-09-779-308-546	Sequence 546, App
19	30	49.2	10	9	US-09-779-308-640	Sequence 640, App
20	30	49.2	10	14	US-10-264-374-57	Sequence 57, Appl
21	30	49.2	10	14	US-10-375-992-57	Sequence 57, Appl
22	30	49.2	10	15	US-10-264-374-57	Sequence 57, Appl
23	30	49.2	10	16	US-10-375-992-57	Sequence 57, Appl
24	30	49.2	10	17	US-10-838-289-593	Sequence 593, App
25	29	47.5	8	13	US-10-010-408-4	Sequence 4, Appli
26	29	47.5	8	15	US-10-149-138-2467	Sequence 2467, Ap
27	29	47.5	8	15	US-10-149-138-3195	Sequence 3195, Ap
28	29	47.5	8	15	US-10-311-129-26	Sequence 26, Appl
29	29	47.5	8	16	US-10-149-138-2467	Sequence 2467, Ap
30	29	47.5	8	16	US-10-149-138-3195	Sequence 3195, Ap
31	29	47.5	9	15	US-10-149-138-855	Sequence 855, App
32	29	47.5	9	15	US-10-149-138-2495	Sequence 2495, App
33	29	47.5	9	15	US-10-149-138-3217	Sequence 3217, Ap
34	29	47.5	9	16	US-10-149-138-4122	Sequence 4122, Ap
35	29	47.5	9	16	US-10-149-138-855	Sequence 855, App
36	29	47.5	9	16	US-10-149-138-2495	Sequence 2495, App
37	29	47.5	9	16	US-10-149-138-3217	Sequence 3217, Ap
38	29	47.5	9	16	US-10-149-138-4122	Sequence 4122, Ap
39	29	47.5	10	9	US-09-765-086-52	Sequence 52, Appl
40	29	47.5	10	10	US-09-572-404B-2757	Sequence 2757, Ap
41	29	47.5	10	10	US-09-572-404B-2759	Sequence 2759, Ap
42	29	47.5	10	10	US-09-572-404B-2761	Sequence 2761, Ap
43	29	47.5	10	10	US-09-572-404B-3780	Sequence 3780, Ap
44	29	47.5	10	14	US-10-264-374-52	Sequence 52, Appl
45	29	47.5	10	14	US-10-375-992-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1

US-09-867-159A-3

Sequence 3, Application US/09867159A

Publication No. US20030104013A1

GENERAL INFORMATION:

APPLICANT: ANTIALIS TERRASSE, GAETAN LORIA, EMILE TREHIN, YVES

TITLE OF INVENTION: Anti-allergic pharmaceutical composition containing at least one

FILE OF INVENTION: and at least one anti-histamine compound

FILE REFERENCE: B112812US-antialis

CURRENT APPLICATION NUMBER: US/09/867,159A

PRIOR FILING DATE: 2001-05-29

PRIOR APPLICATION NUMBER: FR01/04370

PRIOR FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: FR01/05929

PRIOR FILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 10

TYPE: PRT

ORGANISM: Dermatophagoides pteronyssinus

FEATURE:

NAME/KEY: PEPTIDE

LOCATION: (1)..(10)

OTHER INFORMATION: Comprises epitope from cystine protease.

US-09-867-159A-3

Query Match 100.0%; Score 61; DB 10; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.03; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0;

Qy 1 RMOGGCGSCN 10

Db 1 RMOGGCGSCN 10

```
RESULT 2
; US-10-175-833-59
; Sequence 59, Application US/10175833
; Publication No. US20030211981A1
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas Stephen
; APPLICANT: BARTOLOMEO, Maria
; TITLE OF INVENTION: COMPOUNDS AND METHOD FOR THE PREVENTION AND TREATMENT
; TITLE OF INVENTION: OF DIABETIC RETINOPATHY
; FILE REFERENCE: 028724-109
; CURRENT APPLICATION NUMBER: US/10/175,833
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/144,991
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: US 60/058,423
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)
; OTHER INFORMATION: Amino acid 1 is attached by Trig.
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (7)
; OTHER INFORMATION: Amino acid 7 is attached by a hydroxide bond.
; NAME/KEY: DISULFID
; LOCATION: (3)..(6)
; OTHER INFORMATION: Cysteine residues at positions 3 and 6 are
; OTHER INFORMATION: attached by a non-peptidal disulfide bond.
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:peptide derivative
; US-10-175-833-59

Query Match          59.0%; Score 36; DB 15; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GCGGSC 9
Db      1 GCGGSC 6

RESULT 3
; US-10-175-833-60
; Sequence 60, Application US/10175833
; Publication No. US20030211981A1
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas Stephen
; APPLICANT: BARTOLOMEO, Maria
; TITLE OF INVENTION: COMPOUNDS AND METHOD FOR THE PREVENTION AND TREATMENT
; TITLE OF INVENTION: OF DIABETIC RETINOPATHY
; FILE REFERENCE: 028724-109
; CURRENT APPLICATION NUMBER: US/10/175,833
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/144,991
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: US 60/058,423
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)
; OTHER INFORMATION: Amino acid 1 is attached by Nic.

; US-10-175-833-59

Query Match          59.0%; Score 36; DB 15; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GCGGSC 9
Db      1 GCGGSC 6

RESULT 3
; US-10-175-833-60
; Sequence 60, Application US/10175833
; Publication No. US20030211981A1
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas Stephen
; APPLICANT: BARTOLOMEO, Maria
; TITLE OF INVENTION: COMPOUNDS AND METHOD FOR THE PREVENTION AND TREATMENT
; TITLE OF INVENTION: OF DIABETIC RETINOPATHY
; FILE REFERENCE: 028724-109
; CURRENT APPLICATION NUMBER: US/10/175,833
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/144,991
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: US 60/058,423
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)
; OTHER INFORMATION: Amino acid 1 is attached by Nic.
```

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; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (7)
; OTHER INFORMATION: Amino acid 7 is attached by a hydroxide bond.
; NAME/KEY: DISULFIDE
; LOCATION: (3)..(6)
; OTHER INFORMATION: Cysteine residues at positions 3 and 6 are
; OTHER INFORMATION: attached by a non-peptidal disulfide bond.
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:peptide derivative
; US-10-175-833-60

Query Match          59.0%; Score 36; DB 15; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GCGGSC 9
Db      1 GCGGSC 6

RESULT 4
; US-10-175-833-62
; Sequence 62, Application US/10175833
; Publication No. US20030211981A1
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas Stephen
; APPLICANT: BARTOLOMEO, Maria
; TITLE OF INVENTION: COMPOUNDS AND METHOD FOR THE PREVENTION AND TREATMENT
; TITLE OF INVENTION: OF DIABETIC RETINOPATHY
; FILE REFERENCE: 028724-109
; CURRENT APPLICATION NUMBER: US/10/175,833
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/144,991
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: US 60/058,423
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)
; OTHER INFORMATION: Amino acid 1 is attached by Nic.

; US-10-175-833-62

Query Match          59.0%; Score 36; DB 15; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GCGGSC 9
Db      1 GCGGSC 6

RESULT 5
; US-09-287-849-43
; Sequence 43, Application US/09287849
; Patent No. US20020009459A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Alderson, Mark
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; TITLE OF INVENTION: and Their Uses
; FILE REFERENCE: 014058-009020US
; CURRENT APPLICATION NUMBER: US/09/287,849
; CURRENT FILING DATE: 1999-04-07
; PRIOR FILING DATE: 1997-03-13
; PRIOR FILING DATE: 1997-03-13
; PRIOR FILING DATE: 1997-03-13
; PRIOR FILING DATE: 1997-10-01
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-04-07
; PRIOR FILING DATE: 1998-04-07
; PRIOR FILING DATE: 1998-04-07
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:flexible
; OTHER INFORMATION: polylinker
US-09-287-849-43

Query Match          59.0%; Score 36; DB 9; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCGGSC 9
    |||||
Db 3 GCGGSC 8

RESULT 6
US-10-359-460-43
; Sequence 43, Application US/10359460
; Publication No. US20030147911A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Alderson, Mark
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; TITLE OF INVENTION: and Their Uses
; FILE REFERENCE: 014058-009020US
; CURRENT APPLICATION NUMBER: US/10/359,460
; CURRENT FILING DATE: 2003-02-05
; PRIOR FILING DATE: 1999-04-07
; PRIOR FILING DATE: 1999-04-07
; PRIOR FILING DATE: 1997-03-13
; PRIOR FILING DATE: 1997-03-13
; PRIOR FILING DATE: 1997-10-01
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-04-07
; PRIOR FILING DATE: 1998-04-07
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:flexible
; OTHER INFORMATION: polylinker
US-09-287-849-43

Query Match          59.0%; Score 36; DB 9; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCGGSC 9
    |||||
Db 3 GCGGSC 8

RESULT 6
US-10-359-460-43
; Sequence 43, Application US/10359460
; Publication No. US20030147911A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Alderson, Mark
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; TITLE OF INVENTION: and Their Uses
; FILE REFERENCE: 014058-009020US
; CURRENT APPLICATION NUMBER: US/10/359,460
; CURRENT FILING DATE: 2003-02-05
; PRIOR FILING DATE: 1999-04-07
; PRIOR FILING DATE: 1999-04-07
; PRIOR FILING DATE: 1997-03-13
; PRIOR FILING DATE: 1997-03-13
; PRIOR FILING DATE: 1997-10-01
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-04-07
; PRIOR FILING DATE: 1998-04-07
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 9

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:flexible
; OTHER INFORMATION: polylinker
US-10-359-460-43

Query Match          59.0%; Score 36; DB 14; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCGGSC 9
    |||||
Db 3 GCGGSC 8

RESULT 7
US-10-359-459-7
; Sequence 7, Application US/10359459
; Publication No. US20040013677A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Alderson, Mark
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; TITLE OF INVENTION: and Their Uses
; FILE REFERENCE: 014058-009010US
; CURRENT APPLICATION NUMBER: US/10/359,459
; CURRENT FILING DATE: 2003-02-05
; PRIOR FILING DATE: 1998-12-30
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:flexible
; OTHER INFORMATION: polylinker
US-10-359-459-7

Query Match          59.0%; Score 36; DB 15; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCGGSC 9
    |||||
Db 3 GCGGSC 8

RESULT 8
US-10-163-415-2
; Sequence 2, Application US/10163415
; Publication No. US20030129204A1
; GENERAL INFORMATION:
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: SMITH, STUART KEVIN
; APPLICANT: SMITH, WILLIAM DAVID
; APPLICANT: REDMOND, DIANE
; APPLICANT: MURRAY, JACQUELINE
; TITLE OF INVENTION: VACCINES AGAINST HELMINTHIC PARASITES
; FILE REFERENCE: 1181-264
; CURRENT APPLICATION NUMBER: US/10/163,415
; CURRENT FILING DATE: 2002-06-07
; PRIOR FILING DATE: US 08/716418
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: PCT/GB95/00665
; PRIOR FILING DATE: 1995-03-24
; PRIOR APPLICATION NUMBER: GB 9405925.0
; PRIOR FILING DATE: 1994-03-25
; PRIOR APPLICATION NUMBER: GB 9405990.4

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; PRIOR FILING DATE: 1994-03-25
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; NAME/KEY: misc feature
 ; LOCATION: (6)-(6)
 ; OTHER INFORMATION: The 'Xaa' at location 6 stands for Ser.
 ; FEATURE:
 ; OTHER INFORMATION: PCR primer: 508G
 ;
 US-10-163-415-2

Query Match 54.1%; Score 33; DB 14; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.3e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 QGCGGSC 9
 Db 1 QGCGGXC 7

RESULT 9

US-10-678-961B-62
 ; Sequence 62, Application US/10678961B
 ; Publication No. US20050074883A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Slater, Michael R.
 ; APPLICANT: Strauss, Ethan Edward
 ; APPLICANT: Wood, Keith V.
 ; APPLICANT: Hartnett, James Robert
 ; APPLICANT: Promega Corporation
 ; TITLE OF INVENTION: Vectors for Directional Cloning
 ; FILE REFERENCE: 341.023US1
 ; CURRENT APPLICATION NUMBER: US/10/678,961B
 ; CURRENT FILING DATE: 2003-10-03
 ; NUMBER OF SEQ ID NOS: 91
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 62
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: A synthetic peptide
 ;
 US-10-678-961B-62

Query Match 51.6%; Score 31.5; DB 17; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.3e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 4 GCGGSCN 10
 Db 2 GCGG-CN 7

RESULT 10

US-10-702-228A-62
 ; Sequence 62, Application US/10702228A
 ; Publication No. US20050074785A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Slater, Michael R.
 ; APPLICANT: Wood, Keith V.
 ; APPLICANT: Hartnett, James Robert
 ; APPLICANT: Promega Corporation
 ; TITLE OF INVENTION: Vectors for Directional Cloning
 ; FILE REFERENCE: 341.030US1
 ; CURRENT APPLICATION NUMBER: US/10/702,228A
 ; CURRENT FILING DATE: 2003-11-05
 ; PRIOR APPLICATION NUMBER: 10/678,961
 ; PRIOR FILING DATE: 2003-10-03
 ; NUMBER OF SEQ ID NOS: 92

; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 62
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: A synthetic peptide
 ;
 US-10-702-228A-62

Query Match 51.6%; Score 31.5; DB 17; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.3e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 4 GCGGSCN 10
 Db 2 GCGG-CN 7

RESULT 11

US-09-287-849-42
 ; Sequence 42, Application US/09287849
 ; Patent No. US20020009459A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Alderson, Mark
 ; APPLICANT: Campos-Neto, Antonio
 ; APPLICANT: Corixa Corporation
 ; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
 ; FILE REFERENCE: 014058-009020US
 ; CURRENT APPLICATION NUMBER: US/09/287,849
 ; CURRENT FILING DATE: 1999-04-07
 ; PRIOR APPLICATION NUMBER: US 08/818,112
 ; PRIOR FILING DATE: 1997-03-13
 ; PRIOR APPLICATION NUMBER: US 08/942,578
 ; PRIOR FILING DATE: 1997-10-01
 ; PRIOR APPLICATION NUMBER: US 09/025,197
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 09/056,556
 ; PRIOR FILING DATE: 1998-04-07
 ; PRIOR APPLICATION NUMBER: US 09/223,040
 ; PRIOR FILING DATE: 1998-12-30
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 42
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:flexible
 ; OTHER INFORMATION: polylinker
 ;
 US-09-287-849-42

Query Match 49.2%; Score 30; DB 9; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGSC 9
 Db 1 GCGGC 5

RESULT 12

US-10-359-460-42
 ; Sequence 42, Application US/10359460
 ; Publication No. US20030147911A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Alderson, Mark

APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/10/359,460
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 42
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: flexible
OTHER INFORMATION: polylinker
US-10-359-460-42

Query Match 49.2%; Score 30; DB 14; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGSC 9
|||
Db 1 GCGGC 5

RESULT 13
US-10-359-459-6
Sequence 6, Application US/10359459
Publication No. US20040013677A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
FILE REFERENCE: 014058-009010US
CURRENT APPLICATION NUMBER: US/10/359,459
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: flexible
OTHER INFORMATION: polylinker
US-10-359-459-6

Query Match 49.2%; Score 30; DB 15; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGSC 9
|||
Db 1 GCGGC 5

RESULT 14
US-09-765-086-57
Sequence 57, Application US/09765086
Patent No. US20010046498A1
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
APPLICANT: Wadih, Arap
APPLICANT: Bredesen, Dale E.
APPLICANT: Ellerbe, H. Michael
TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
TITLE OF INVENTION: Pro-Apoptotic Activity
FILE REFERENCE: P-LJ 3844
CURRENT APPLICATION NUMBER: US/09/765,086
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US 09/489,582
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 235
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 57
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-09-765-086-57

Query Match 49.2%; Score 30; DB 9; Length 10;
Best Local Similarity 80.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGSCN 10
|||
Db 1 CGECN 5

RESULT 15
US-09-779-308-222
Sequence 222, Application US/09779308
Patent No. US20020150972A1
GENERAL INFORMATION:
APPLICANT: Mary Faris
APPLICANT: Daniel E.H. Afar
APPLICANT: Pia M. Challita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Elana Levin
APPLICANT: Steve Chappell Mitchell
APPLICANT: Ava Jakobovits
TITLE OF INVENTION: 34PD7: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
FILE REFERENCE: 129.4USU1
CURRENT APPLICATION NUMBER: US/09/779,308
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 60/181,020
PRIOR FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 718
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 222
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-779-308-222

Query Match 49.2%; Score 30; DB 9; Length 10;
Best Local Similarity 71.4%; Pred. No. 7.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RMOGCGC 7
|||
Db 1 RLQGGAG 7

Search completed: May 19, 2005, 18:19:58
Job time : 90.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:53:34 ; Search time 29.5 Seconds
(without alignments)
25.305 Million cell updates/sec

Title: US-09-867-159A-3

Perfect score: 61

Sequence: 1 RMQGGCGSCN 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 115750

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	59.0	7	4	US-09-144-991B-59
2	36	59.0	7	4	US-09-144-991B-60
3	36	59.0	7	4	US-09-144-991B-62
4	36	59.0	9	4	US-09-470-191-94
5	36	59.0	9	4	US-09-223-040-7
6	36	59.0	9	4	US-09-287-849-43
7	31	50.8	8	2	US-08-835-099A-3
8	31	50.8	8	3	US-09-157-349-3
9	31	50.8	8	3	US-08-779-072A-6
10	30	49.2	6	4	US-09-470-191-93
11	30	49.2	6	4	US-09-223-040-6
12	30	49.2	6	4	US-09-287-849-42
13	30	49.2	8	3	US-08-779-072A-1
14	30	49.2	10	2	US-08-361-864-36
15	30	49.2	10	2	US-08-902-367-7
16	30	49.2	10	3	US-08-535-170-9
17	30	49.2	10	3	US-09-139-802-57
18	30	49.2	10	4	US-09-659-786-57
19	30	49.2	10	4	US-08-926-914-57
20	29	47.5	9	1	US-08-482-880-8
21	29	47.5	9	2	US-08-273-274-8
22	29	47.5	9	2	US-08-475-041-8
23	29	47.5	9	2	US-08-484-773-8
24	29	47.5	10	2	US-08-335-832-8
25	29	47.5	10	3	US-09-141-127-2
26	29	47.5	10	3	US-09-139-802-52
27	29	47.5	10	4	US-09-659-786-52

28	29	47.5	10	4	US-08-926-914-52	Sequence 52, Appl
29	28	45.9	5	1	US-08-467-607-10	Sequence 10, Appl
30	28	45.9	5	2	US-08-469-362-10	Sequence 10, Appl
31	28	45.9	5	2	US-08-850-392-10	Sequence 10, Appl
32	28	45.9	6	4	US-09-982-704-9	Sequence 9, Appl
33	28	45.9	7	3	US-08-827-171B-13	Sequence 13, Appl
34	28	45.9	7	4	US-09-588-995A-111	Sequence 111, Appl
35	28	45.9	7	4	US-09-598-062-13	Sequence 13, Appl
36	28	45.9	8	1	US-08-526-710-28	Sequence 28, Appl
37	28	45.9	8	3	US-08-862-855-28	Sequence 28, Appl
38	28	45.9	8	3	US-09-226-985-28	Sequence 28, Appl
39	28	45.9	8	3	US-09-227-906-28	Sequence 28, Appl
40	28	45.9	8	4	US-09-228-866-28	Sequence 28, Appl
41	28	45.9	9	3	US-08-997-802-10	Sequence 10, Appl
42	28	45.9	9	3	US-08-997-802-11	Sequence 11, Appl
43	28	45.9	10	3	US-09-139-802-32	Sequence 32, Appl
44	28	45.9	10	4	US-09-659-786-32	Sequence 32, Appl
45	28	45.9	10	4	US-08-926-914-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-09-144-991B-59
; Sequence 59, Application US/09144991B
; Patent No. 6440933
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas Stephen
; APPLICANT: BARTOLOMEO, Maria
; TITLE OF INVENTION: COMPOUNDS AND METHOD FOR THE PREVENTION AND TREATMENT
; TITLE OF INVENTION: OF DIABETIC RETINOPATHY
; FILE REFERENCE: 028724-109
; CURRENT APPLICATION NUMBER: US/09/144,991B
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: US 60/058,423
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)
; OTHER INFORMATION: Amino acid 1 is attached by Trig.
; NAME/KEY: BINDING
; LOCATION: (7)
; OTHER INFORMATION: Amino acid 7 is attached by a hydroxide bond.
; NAME/KEY: DISULFID
; LOCATION: (3)..(6)
; OTHER INFORMATION: Cysteine residues at positions 3 and 6 are
; OTHER INFORMATION: attached by a non-peptidic disulfide bond.
; OTHER INFORMATION: Description of Unknown organism:peptide derivative
US-09-144-991B-59

Query Match 59.0%; Score 36; DB 4; Length 7;

Best Local Similarity 83.3%; Pred. No. 4.1e+05;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCGGSC 9
|||
Db 1 GCGGCG 6

RESULT 2

US-09-144-991B-60
; Sequence 60, Application US/09144991B
; Patent No. 6440933
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas Stephen
; APPLICANT: BARTOLOMEO, Maria

;; TITLE OF INVENTION: COMPOUNDS AND METHOD FOR THE PREVENTION AND TREATMENT
;; FILE REFERENCE: 028724-109
;; CURRENT APPLICATION NUMBER: US/09/144,991B
;; CURRENT FILING DATE: 1998-09-01
;; PRIOR APPLICATION NUMBER: US 60/058,423
;; PRIOR FILING DATE: 1997-09-10
;; NUMBER OF SEQ ID NOS: 65
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 60
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Unknown
;; FEATURE:
;; NAME/KEY: BINDING
;; LOCATION: (1)
;; OTHER INFORMATION: Amino acid 1 is attached by Nic.
;; NAME/KEY: BINDING
;; LOCATION: (7)
;; OTHER INFORMATION: Amino acid 7 is attached by a hydroxide bond.
;; NAME/KEY: DISULFIDE
;; LOCATION: (3)..(6)
;; OTHER INFORMATION: Cysteine residues at positions 3 and 6 are
;; attached by a non-peptidic disulfide bond.
;; OTHER INFORMATION: Description of Unknown Organism:peptide derivative
US-09-144-991B-60

Query Match 59.0%; Score 36; DB 4; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCGGSC 9
|||
Db 1 GCGGCG 6

RESULT 3
US-09-144-991B-62
;; Sequence 62, Application US/09144991B
;; Patent No. 6440933
;; GENERAL INFORMATION:
;; APPLICANT: BODOR, Nicholas Stephen
;; APPLICANT: BARTOLOMO, Maria
;; TITLE OF INVENTION: COMPOUNDS AND METHOD FOR THE PREVENTION AND TREATMENT
;; FILE REFERENCE: 028724-109
;; CURRENT APPLICATION NUMBER: US/09/144,991B
;; CURRENT FILING DATE: 1998-09-01
;; PRIOR APPLICATION NUMBER: US 60/058,423
;; PRIOR FILING DATE: 1997-09-10
;; NUMBER OF SEQ ID NOS: 65
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 62
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Unknown
;; FEATURE:
;; NAME/KEY: BINDING
;; LOCATION: (1)
;; OTHER INFORMATION: Amino acid 1 is attached by Nic.
;; NAME/KEY: BINDING
;; LOCATION: (7)
;; OTHER INFORMATION: Amino acid 7 is attached by a hydroxide bond.
;; NAME/KEY: DISULFID
;; LOCATION: (3)..(6)
;; OTHER INFORMATION: Cysteine residues at positions 3 and 6 are
;; attached by a non-peptidic disulfide bond.
;; OTHER INFORMATION: Description of Unknown Organism:peptide derivative
US-09-144-991B-62

Query Match 59.0%; Score 36; DB 4; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCGGSC 9
|||
Db 1 GCGGCG 6

RESULT 4
US-09-470-191-94
;; Sequence 94, Application US/09470191
;; Patent No. 6465633
;; GENERAL INFORMATION:
;; APPLICANT: Skeiky, Yasir
;; APPLICANT: Corixa Corporation
;; TITLE OF INVENTION: Compositions and Methods of Their Use in
;; the Treatment, Prevention and Diagnosis of Tuberculosis
;; FILE REFERENCE: 014058-008910US
;; CURRENT APPLICATION NUMBER: US/09/470,191
;; CURRENT FILING DATE: 1999-12-23
;; PRIOR APPLICATION NUMBER: US 60/113,952
;; PRIOR FILING DATE: 1998-12-24
;; NUMBER OF SEQ ID NOS: 97
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 94
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: flexible polylinker
US-09-470-191-94

Query Match 59.0%; Score 36; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCGGSC 9
|||
Db 3 GCGGCG 8

RESULT 5
US-09-223-040-7
;; Sequence 7, Application US/09223040
;; Patent No. 6544522
;; GENERAL INFORMATION:
;; APPLICANT: Skeiky, Yasir
;; APPLICANT: Alderson, Mark
;; APPLICANT: Campos-Neto, Antonio
;; APPLICANT: Corixa Corporation
;; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
;; FILE REFERENCE: 014058-009010US
;; CURRENT APPLICATION NUMBER: US/09/223,040
;; CURRENT FILING DATE: 1998-12-30
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 7
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:flexible
;; OTHER INFORMATION: polylinker
US-09-223-040-7

Query Match 59.0%; Score 36; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCGGSC 9
|||
Db 3 GCGGCG 8

RESULT 6
US-09-287-849-43
; Sequence 43, Application US/09287849
; Patent No. 6627198
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Alderson, Mark
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; TITLE OF INVENTION: and Their Uses
; FILE REFERENCE: 014058-009020US
; CURRENT APPLICATION NUMBER: US/09/287,849
; CURRENT FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: US 08/818,112
; PRIOR FILING DATE: 1997-03-13
; PRIOR APPLICATION NUMBER: US 08/942,578
; PRIOR FILING DATE: 1997-10-01
; PRIOR APPLICATION NUMBER: US 09/025,197
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 09/056,556
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 09/223,040
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: flexible
; OTHER INFORMATION: polylinker
US-09-287-849-43

Query Match 59.0%; Score 36; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCGGSC 9
||| |
Db 3 GCGGSC 8

RESULT 7
US-08-835-099A-3
; Sequence 3, Application US/08835099A
; Patent No. 5874277
; GENERAL INFORMATION:
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: NISHI, Kazuori
; APPLICANT: KAWAMOTO, Tomohiro
; TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION
; TITLE OF INVENTION: AND USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,099A
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 083649/1996
; FILING DATE: 05-APR-1996
; APPLICATION NUMBER: 97105508.2
; FILING DATE: 03-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 47342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-835-099A-3
Query Match 50.8%; Score 31; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 QGCGSC 9
||| |
Db 2 QGGLGDC 8

RESULT 8
US-09-157-349-3
; Sequence 3, Application US/09157349
; Patent No. 6068990
; GENERAL INFORMATION:
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: NISHI, Kazuori
; APPLICANT: KAWAMOTO, Tomohiro
; TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION
; TITLE OF INVENTION: AND USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,349
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/835,099
; FILING DATE:
; APPLICATION NUMBER: 97105508.2
; FILING DATE: 03-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 47342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

```
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-157-349-3

Query Match          50.8%; Score 31; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGCGSC 9
Db 2 QGGLGDC 8

RESULT 9
US-08-779-072A-6
; Sequence 6, Application US/08779072A
; Patent No. 6180767
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric
; APPLICANT: Basu, Soumitra
; TITLE OF INVENTION: PEPTIDE NUCLEIC ACID CONJUGATES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,072A
; FILING DATE: January 7, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,747
; FILING DATE: January 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 6180767e
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-779-072A-6

Query Match          50.8%; Score 31; DB 3; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCGCSC 9
Db 3 GGCAAC 8

RESULT 10
US-09-470-191-93
; Sequence 93, Application US/09470191
; Patent No. 6465633

; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods of Their Use in
; FILE REFERENCE: 014058-008910US
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113,952
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 93
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: flexible polylinker
US-09-470-191-93

Query Match          49.2%; Score 30; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGSC 9
Db 1 GCGGC 5

RESULT 11
US-09-223-040-6
; Sequence 6, Application US/09223040
; Patent No. 6544522
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Alderson, Mark
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; FILE REFERENCE: 014058-009010US
; CURRENT APPLICATION NUMBER: US/09/223,040
; CURRENT FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:flexible
; OTHER INFORMATION: polylinker
US-09-223-040-6

Query Match          49.2%; Score 30; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGSC 9
Db 1 GCGGC 5

RESULT 12
US-09-287-849-42
; Sequence 42, Application US/09287849
; Patent No. 6627198
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Alderson, Mark
; APPLICANT: Campos-Neto, Antonio
```

; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; FILE REFERENCE: and Their Uses
; CURRENT APPLICATION NUMBER: 014058-009020US
; CURRENT FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: US 08/818,112
; PRIOR FILING DATE: 1997-03-13
; PRIOR APPLICATION NUMBER: US 08/942,578
; PRIOR FILING DATE: 1997-10-01
; PRIOR APPLICATION NUMBER: US 09/025,197
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 09/056,556
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 09/223,040
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:flexible
; OTHER INFORMATION: polylinker
US-09-287-849-42

Query Match 49.2%; Score 30; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.le+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGSC 9
Db 1 GCGGC 5

RESULT 13

US-08-779-072A-1
; Sequence 1, Application US/08779072A
; Patent No. 6180767

; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric
; APPLICANT: Basu, Sumittra
; TITLE OF INVENTION: PEPTIDE NUCLEIC ACID CONJUGATES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,072A
; FILING DATE: January 7, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,747
; FILING DATE: January 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 6180767e
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-779-072A-1

Query Match 49.2%; Score 30; DB 3; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.le+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCGSC 9
Db 3 GCGSC 8

RESULT 14

US-08-361-864-36
; Sequence 36, Application US/08361864
; Patent No. 5977064
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Multimeric Polyvalent Antithrombotic
; TITLE OF INVENTION: Agents
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,864
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/955,466A
; FILING DATE: 19921002
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5977064han, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,668
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..5
; OTHER INFORMATION: /label= Cyclic
; OTHER INFORMATION: /note= "The sidechain sulfur of the 1st cysteine
; OTHER INFORMATION: is protected by an -CH2CO- group, that also forms
; OTHER INFORMATION: an amide bond with the N-terminus; the Y is the D
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6..8
; OTHER INFORMATION: /label= Tc-99m-binding
; OTHER INFORMATION: /note= "The sidechain sulfur atom of each cysteine
; OTHER INFORMATION: is protected by an acetamido group; the C-terminal
; OTHER INFORMATION: cysteine is an amide"

US-08-361-864-36

Query Match 49.2%; Score 30; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 QGCGSC 9
:|:|:
Db 2 RGDCGC 8

RESULT 15

US-08-902-367-7
; Sequence 7, Application US/08902367
; Patent No. 597845
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R.
; TITLE OF INVENTION: Radiolabeled Compounds for Thrombus
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive Seventh Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,367
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/462,668
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5997845nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 90,1104-W
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312 913 0001
; TELEFAX: 312 913 0002
; TELEX:

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..3
; OTHER INFORMATION: /label= D-Tyr
; OTHER INFORMATION: /note= "The tyrosine residue is in the D-stereo-
; OTHER INFORMATION: chemical configuration"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..5
; OTHER INFORMATION: /label= Cyclic
; OTHER INFORMATION: /note= "The sidechain sulfur of the Cys
; OTHER INFORMATION: residue is covalently linked to the amino
; OTHER INFORMATION: terminus by a -CH2CO- group."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8..10
; OTHER INFORMATION: /label= Tc-99m-chelator
; OTHER INFORMATION: /note= "The sidechain sulfur atoms of both Cys

; OTHER INFORMATION: residues are each protected with an
; OTHER INFORMATION: acetamidomethyl group"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /label= Amide
; OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
; OTHER INFORMATION: amide"
; US-08-902-367-7

Query Match 49.2%; Score 30; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 QGCGSC 9
:|:|:
Db 2 RGDCGC 8

Search completed: May 19, 2005, 18:11:52
Job time : 31.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:50:19 ; Search time 12 Seconds
(without alignments)
80.181 Million cell updates/sec

Title: US-09-867-159A-4

Perfect score: 55

Sequence: 1 QPNYHAVNIV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	32.7	10	2 S65387	cytochrome-C oxida
2	17	30.9	8	2 JS0316	leucokinin VI - Ma
3	16	29.1	7	1 NYPG7	hypothalamic hepta
4	16	29.1	9	2 PT0285	Ig heavy chain CRD
5	16	29.1	9	2 S55696	phosphoenolpyruvat
6	16	29.1	10	2 A43405	6-phosphofructo-2-
7	16	29.1	10	2 S33844	alpha-2-macroglobu
8	16	29.1	10	2 PT0291	Ig heavy chain CRD
9	16	29.1	10	2 A59272	peptide-N4-(N-acet
10	16	29.1	10	2 S23307	neurokinin A - rat
11	16	29.1	10	2 S23186	neurokinin A - Atl
12	15	27.3	7	2 A38081	amine oxidase (cop
13	15	27.3	7	2 A15398	choline oxidase (E
14	15	27.3	8	2 A44960	neuropeptide Led-C
15	15	27.3	8	2 B44960	neuropeptide Led-C
16	15	27.3	8	2 S08995	hypertrehalosemic
17	15	27.3	8	2 S08996	hypertrehalosemic
18	15	27.3	8	2 A49823	adipokinetic hormo
19	15	27.3	8	2 B49823	adipokinetic hormo
20	15	27.3	8	2 S15422	adipokinetic hormo
21	15	27.3	8	2 A43976	hypertrehalosemic
22	15	27.3	8	2 B43976	hypertrehalosemic
23	15	27.3	8	2 A58641	adipokinetic hormo
24	15	27.3	8	2 A05169	neuropeptide M-I -
25	15	27.3	9	2 S70345	amine oxidase (cop
26	15	27.3	9	2 PT0270	Ig heavy chain CRD
27	15	27.3	9	2 S13889	phosphoenolpyruvat
28	15	27.3	9	2 S77984	cytochrome-C oxida
29	15	27.3	10	1 ECLQAM	tachykinin IV - mi

30 15 27.3 10 2 JC1416 hypertrehalosemic
31 15 27.3 10 2 S09138 hypertrehalosemic
32 15 27.3 10 2 PT0213 T-cell receptor al
33 15 27.3 10 2 JQ0943 hypothetical 1.3K
34 14 25.5 6 2 PQ0008 angiotensin-conver
35 14 25.5 7 2 S71867 glutathione transf
36 14 25.5 8 2 A59028 MHC class I histoc
37 14 25.5 9 2 A61230 calsequestrin, car
38 14 25.5 9 2 C41170 photosystem II pro
39 14 25.5 9 2 PT0288 Ig heavy chain CRD
40 14 25.5 9 2 PT0324 Ig heavy chain CRD
41 14 25.5 9 2 D41978 callipressamide 4 -
42 14 25.5 10 2 S10926 inhibit beta-A cha
43 14 25.5 10 2 A60647 neuromedin C - bov
44 13 23.6 6 2 A44916 mosquitoicidal toxi
45 13 23.6 7 2 S21230 dermorphin (Trp-4,

ALIGNMENTS

RESULT 1

S65387

cytochrome-C oxidase (EC 1.9.3.1) chain VII b, cardiac - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004

C;Accession: S65387; S65386

R;Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.

Eur. J. Biochem. 230, 235-241, 1995

A;Title: Cytochrome-C oxidase in developing rat heart. Enzymic properties and amino-term

A;Reference number: S65372; MUID:95324529; PMID:7601105

A;Accession: S65387

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <SCH>

A;Cross-references: UNIPROT:P80431

A;Accession: S65386

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <SC2>

C;Keywords: cardiac muscle; heart; oxidoreductase

Query Match 32.7%; Score 18; DB 2; Length 10;

Best Local Similarity 50.0%; Pred. No. 1.6e+03;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PNVH 5

Db 7 PTFH 10

RESULT 2

JS0316

leucokinin VI - Madeira cockroach

C;Species: Leucophaea madeirae (Madeira cockroach)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C;Accession: JS0316

R;Holman, G.M.; Cook, B.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 88, 27-30, 1987

A;Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotropic

A;Reference number: JS0315

A;Accession: JS0316

A;Molecule type: protein

A;Residues: 1-8 <HOL>

A;Cross-references: UNIPROT:P19988

C;Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile act

C;Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 30.9%; Score 17; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPNYHA 6
| : : :
Db 1 QSFHFS 6

RESULT 3
NYPG7
hypothalamic heptapeptide - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C:Accession: A01417
R;Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong, H.H.; Metab. Res. 13, 228-232, 1981
A:Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-releasing activity
A:Reference number: A01417; MUID:81213980; PMID:6263778
A:Accession: A01417
A:Molecule type: protein
A:Residues: 1-7 <CHA>
A:Cross-references: UNIPROT:P01153
C:Superfamily: hypothalamic heptapeptide
C:Keywords: hypothalamus

Query Match 29.1%; Score 16; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YHA 6
| : :
Db 3 YHS 5

RESULT 4
PT0285
Ig heavy chain CRD3 region (clone 4-100A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0285
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J_H gene segments in the development of the B cell repertoire
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0285
A:Molecule type: DNA
A:Residues: 1-9 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 29.1%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PNYH 5
| : :
Db 4 PTYH 7

RESULT 5
S55696
phosphoenolpyruvate carboxykinase - Trypanosoma brucei
C:Species: Trypanosoma brucei
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S55696
R;Hunt, M.; Koehler, P. Biochim. Biophys. Acta 1249, 15-22, 1995
A:Title: Purification and characterization of phosphoenolpyruvate carboxykinase from Trypanosoma brucei
A:Reference number: S55696; MUID:95284106; PMID:7766679
A:Accession: S55696
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <HUN>
A:Cross-references: UNIPROT:Q7M355

Query Match 29.1%; Score 16; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QPNYH 5
| : :
Db 1 QPIIH 5

RESULT 6
A43405
6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2,6-bisphosphate 2-phosphatase (EC 3.1.3.1)
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: A43405
R;Ventura, F.; Rosa, J.L.; Ambrosio, S.; Palkis, S.J.; Bartons, R. J. Biol. Chem. 267, 17939-17943, 1992
A:Title: Bovine brain 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase. Evidence for a single protein with two distinct activities
A:Reference number: A43405; MUID:92388154; PMID:1325453
A:Accession: A43405
A:Molecule type: protein
A:Residues: 1-10 <VEN>
A:Cross-references: UNIPROT:Q7M313
C:Superfamily: 6-phosphofructo-2-kinase / fructose-2,6-bisphosphate 2-phosphatase; phosphotransferase
C:Keywords: phosphoric monoester hydrolase; phosphotransferase

Query Match 29.1%; Score 16; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QPNYH 5
| : :
Db 1 QVNH 5

RESULT 7
S33844
alpha-2-macroglobulin - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 22-Nov-1993 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: S33844
R;Warburton, M.J.; Coles, B.; Dundas, S.R.; Gusterson, B.A.; O'Hare, M.J. Eur. J. Biochem. 214, 803-809, 1993
A:Title: Hydrocortisone induces the synthesis of alpha(2)-macroglobulin by rat mammary gland
A:Reference number: S33843; MUID:93307297; PMID:7686489
A:Accession: S33844
A:Molecule type: protein
A:Residues: 1-10 <WAR>
C:Superfamily: alpha-2-macroglobulin
C:Keywords: glycoprotein; plasma; proteinase inhibitor; thiolester bond

Query Match 29.1%; Score 16; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPNY 4
| : :
Db 6 EPQY 9

RESULT 8
PT0291
Ig heavy chain CRD3 region (clone 4-115B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0291
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J_H gene segments in the development of the B cell repertoire
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0291
A:Molecule type: DNA
A:Residues: 1-10 <YAM>

A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 29.1%; Score 16; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PNYH 5
| |
Db 4 PTY 7

RESULT 9

A59272
peptide-N4- (N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, large chain
N;Alternate names: peptide N-glycosidase
C;Species: Prunus dulcis var. sativa (sweet almond)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: A59272
R;Altman, F.; Paschinger, K.; Dalik, T.; Vorauer, K.
Eur. J. Biochem. 252, 118-123, 1998
A;Title: Characterisation of peptide-N4- (N-acetyl-beta-glucosaminyl)asparagine amidase A
A;Reference number: A59272; MUID:98181894; PMID:9523720
A;Accession: A59272
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <ALT>
A;Cross-references: UNIPROT:P81899
C;Keywords: hydrolase

Query Match 29.1%; Score 16; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.8e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YHA 6
| |
Db 5 YHS 7

RESULT 10

S23307
neurokinin A - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
C;Accession: S23307
R;Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod
A;Reference number: S23186; MUID:92298992; PMID:1376687
A;Accession: S23307
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <JEN>
A;Cross-references: UNIPROT:P28500

Query Match 29.1%; Score 16; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 HAVN 8
| |
Db 1 HKIN 4

RESULT 11

S23186
neurokinin A - Atlantic cod
C;Species: Gadus morhua (Atlantic cod)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
C;Accession: S23186
R;Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23186
A;Molecule type: protein
A;Residues: 1-10 <JEN>
A;Cross-references: UNIPROT:P28500
A;Experimental source: brain
C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gas.
A;Note: neurokinin A is derived by post-translational processing of preprotachykinin A
C;Keywords: neuropeptide; amidated carboxyl end; tachykinin
F;10/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 29.1%; Score 16; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 HAVN 8
| |
Db 1 HKIN 4

RESULT 12

A38081
amine oxidase (copper-containing) (EC 1.4.3.6) - yeast (*Pichia angusta*) (fragment)
C;Species: *Pichia angusta*
C;Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 20-Apr-2000
C;Accession: A38081
R;Mu, D.; Janes, S.M.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Klinman, J.P.
J. Biol. Chem. 267, 7979-7982, 1992
A;Title: Tyrosine codon corresponds to topa quinone at the active site of copper amine o.
A;Reference number: A38081; MUID:92235001; PMID:1569055
A;Accession: A38081
A;Molecule type: protein
A;Residues: 1-7 <MUA>
C;Keywords: copper; oxidoreductase; quinoprotein; topaquinone
F;4/Modified site: topaquinone (Tyr) #status experimental

Query Match 27.3%; Score 15; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 NYHAV 7
| |
Db 3 NYEV 7

RESULT 13

A15398
choline oxidase (EC 1.1.3.17) - *Alcaligenes* sp. (tentative sequence) (fragment)
C;Species: *Alcaligenes* sp.
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A15398
R;Ohta-Fukuyama, M.; Miyake, Y.; Emi, S.; Yamano, T.
J. Biochem. 88, 197-203, 1980
A;Title: Identification and properties of the prosthetic group of choline oxidase from *A*
A;Reference number: A15398; MUID:81006769; PMID:6997283
A;Accession: A15398
A;Molecule type: protein
A;Residues: 1-7 <OHT>
A;Cross-references: UNIPROT:P16101
C;Keywords: oxidoreductase

Query Match 27.3%; Score 15; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PNY 4
| |
Db 3 PNH 5

RESULT 14

A44960

neuropeptide Led-CC-I - Colorado potato beetle
 C;Species: Leptinotarsa decemlineata (Colorado potato beetle)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: A44960
 R;Gaede, G.; Kellner, R.
 Peptides 10, 1287-1289, 1989
 A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and
 A;Reference number: A44960; MUID:90160053; PMID:2576128
 A;Accession: A44960
 A;Molecule type: protein
 A;Residues: 1-8 <GAE>
 A;Cross-references: UNIPROT:P04548
 C;Superfamily: adipokinetic hormone
 C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 27.3%; Score 15; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. NO. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PNY 4
 ||:
 Db 6 PNW 8

RESULT 15

B44960
 neuropeptide Led-CC-II - Colorado potato beetle
 C;Species: Leptinotarsa decemlineata (Colorado potato beetle)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: B44960
 R;Gaede, G.; Kellner, R.
 Peptides 10, 1287-1289, 1989
 A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and
 A;Reference number: A44960; MUID:90160053; PMID:2576128
 A;Accession: B44960
 A;Molecule type: protein
 A;Residues: 1-8 <GAE>
 A;Cross-references: UNIPROT:P04549
 C;Superfamily: adipokinetic hormone
 C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 27.3%; Score 15; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. NO. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PNY 4
 ||:
 Db 6 PNW 8

Search completed: May 19, 2005, 17:59:35
 Job time : 14 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:54:20 ; Search time 111 Seconds
(without alignments)
46.133 Million cell updates/sec

Title: US-09-867-159A-4
Perfect score: 55
Sequence: 1 QPNYHAVNIV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 2548

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	23	41.8	10	2 Q8J0C2	Q8j0c2 encephalito
2	20	36.4	10	2 Q9UCQ8	Q9ucq8 homo sapien
3	19	34.5	9	2 P90359	P90359 barley mild
4	19	34.5	10	2 Q6R7V4	Q6r7v4 carlia zuma
5	18	32.7	9	1 BS43 SERPL	P83375 serratia pl
6	18	32.7	9	2 Q08979	Q08979 mus musculus
7	18	32.7	10	2 Q7RGV8	Q7rgv8 plasmodium
8	18	32.7	10	2 P82438	P82438 nicotiana t
9	17	30.9	7	1 FAR4 PANRE	P41875 panagrellus
10	17	30.9	8	1 LCK6 LEUMA	P19988 leucophaea
11	17	30.9	10	2 Q9UCF0	Q9ucr0 homo sapien
12	17	30.9	10	2 Q7RSI4	Q7rsi4 plasmodium
13	17	30.9	10	2 Q8QE18	Q8qe18 human immun
14	16	29.1	7	1 HY7 PIG	P01153 sus scrofa
15	16	29.1	7	2 P72081	P72081 nocardia la
16	16	29.1	8	1 ALL1 CYDPO	P82152 cydia pomon
17	16	29.1	8	1 FAR1 PANRE	P41872 panagrellus
18	16	29.1	8	2 Q9UDZ4	Q9udz4 homo sapien
19	16	29.1	8	2 Q9UMH9	Q9umh9 homo sapien
20	16	29.1	8	2 P83158	P83158 arabidosa sp
21	16	29.1	9	1 FAR2 PANRE	P41873 panagrellus
22	16	29.1	9	2 Q7M3S5	Q7m3s5 trypanosoma
23	16	29.1	9	2 Q9TWX7	Q9twx7 manduca sex
24	16	29.1	9	2 Q6XFPV2	Q6xfv2 nectarinia
25	16	29.1	9	2 Q47410	Q47410 escherichia
26	16	29.1	9	2 Q9K4M6	Q9k4m6 staphylococ
27	16	29.1	10	1 PNAL PRUDU	P81899 prunus dulc
28	16	29.1	10	1 TKNB ONCMY	P28500 oncorhynch
29	16	29.1	10	2 Q9UCQ4	Q9ucq4 homo sapien
30	16	29.1	10	2 Q7M3I3	Q7m3i3 bos taurus
31	16	29.1	10	2 Q9TS43	Q9ts43 sus scrofa

32	16	29.1	10	2 Q6XFW8	Q6xfw8 aethopyga b
33	16	29.1	10	2 Q86580	Q86580 simian para
34	15	27.3	7	1 CHOX ALCSP	P16101 alcaligenes
35	15	27.3	8	1 AKH GEOST	P84241 geotrupes s
36	15	27.3	8	1 AKH MELML	P84240 melolontha
37	15	27.3	8	1 AKH PACMA	P84242 pachnoda ma
38	15	27.3	8	1 HTFI PERAM	P04548 periplaneta
39	15	27.3	8	1 HTF2 TENNO	P04549 periplaneta
40	15	27.3	8	1 HTF TENNO	P67789 tenebrio mo
41	15	27.3	8	1 HTF ZOPRU	P67790 zophobas ru
42	15	27.3	8	2 Q15888	Q15888 homo sapien
43	15	27.3	8	2 Q8IUB8	Q8iub8 homo sapien
44	15	27.3	8	2 Q35792	Q35792 saccharomyc
45	15	27.3	8	2 Q6Y2F2	Q6y2f2 citrus sine

ALIGNMENTS

RESULT 1
Q8J0C2 PRELIMINARY; PRT; 10 AA.
AC Q8J0C2;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hsp70 (Fragment).
OS Encephalitozoon hellem.
OC Eukaryota; Fungi; Microsporidia; Unikaryoniidae; Encephalitozoon.
OX NCBI_TaxID=27973;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PV6/95, and PV7/95;
RX MEDLINE=22838663; PubMed=12958242;
RA Haro M., Del Aguila C., Fenoy S., Henriques-Gil N.;
RT "Intraspecies genotype variability of the microsporidian parasite
J. Clin. Microbiol. 41:4166-4171(2003).
RL EMBL; AY171238; AAN73415.1; -;
DR EMBL; AY171239; AAN73417.1; -;
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1100 MW; 107C0D472DD44DD4 CRC64;

Query Match 41.8%; Score 23; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 9.5e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PNYHAVN 8
||| :||
Db 2 PNANALN 8

RESULT 2
Q9UCQ8 PRELIMINARY; PRT; 10 AA.
AC Q9UCQ8;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92129337; PubMed=1733949;
RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schifmann E., Liotta L.A.;
RT "Identification, purification, and partial sequence analysis of
autotaxin, a novel motility-stimulating protein.";
RL J. Biol. Chem. 267:2524-2529(1992).
DR GO; GO:0006928; P:cell motility; NAS.

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FT NON TER 1
FT NON TER 10
SQ SEQUENCE 10 AA; 1171 MW; 736F44577AF1B2CB CRC64;

Query Match 36.4%; Score 20; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

QY 2 PNY 4
DB 7 PNY 9

RESULT 3
P90359 ID P90359 PRELIMINARY; PRT; 9 AA.
AC P90359;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE Polypeptide (Fragment)
OS Barley mild mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Bymovirus.
OX NCBI_TaxID=12466;
RN [1]
RP SEQUENCE FROM N.A.
RA Peerenboom E., Jacobi V., Cartwright E.J., Adams M.J., Steinbiss H.H.,
RA Antoniw J.F.;
RA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RW EMBL; X96970; CAA65658.1; -.
KW Polyprotein.
FT NON TER 1
SQ SEQUENCE 9 AA; 1177 MW; C40404473401F1B6 CRC64;

Query Match 34.5%; Score 19; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PNYHAVN 8
DB 1 POTHRLN 7

RESULT 4
Q6R7V4 ID Q6R7V4 PRELIMINARY; PRT; 10 AA.
AC Q6R7V4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
GN Name=GAPDH;
OS Carlia zuma.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
OC Scincidae; Carlia.
OX NCBI_TaxID=260893;
RN [1]
RP SEQUENCE FROM N.A.
RA Dolman G., Phillips B.;
RT "Single copy nuclear DNA markers characterized for comparative
RT phylogeography in Australian wet tropics rainforest skinks.";
RL Mol. Ecol. Notes 4:185-187(2004).
DR EMBL; AY508912; AAS09890.1; -.
FT NON TER 1
FT NON TER 10
SQ SEQUENCE 10 AA; 1171 MW; 9D0ABB2322C9C1EA CRC64;

Query Match 34.5%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.9e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

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QY 3 NYHAVNIV 10
DB 2 NDHFVKLV 9

RESULT 5
BS43_SERPL ID BS43_SERPL STANDARD; PRT; 9 AA.
AC P83375;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bacteriocin serracin P 43 kDa subunit (Fragment).
OS Serratia plymuthica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=82996;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC STRAIN=J7;
RX MEDLINE=22293561; PubMed=12406768;
RA Jabrane A., Sabri A., Compare P., Jacques P., Vandenberghe I.,
RA Van Beeumen J., Thonart P.;
RT "Characterization of serracin P, a phage-tail-like bacteriocin, and
RT its activity against Erwinia amylovora, the fire blight pathogen.";
RL Appl. Environ. Microbiol. 68:5704-5710(2002).
CC -!- FUNCTION: Major component of a prophage tail sheath (Probable).
CC -!- FUNCTION: Antibacterial activity against Gram-negative bacterium
CC E. amylovora.
CW Antibiotic; Bacteriocin; Direct protein sequencing.
FT NON TER 9
SQ SEQUENCE 9 AA; 1095 MW; 1E66D412C871E1FB CRC64;

Query Match 32.7%; Score 18; DB 1; Length 9;
Best Local Similarity 28.6%; Pred. No. 1.6e+06;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 YHAVNIV 10
DB 3 HHGVRVL 9

RESULT 6
O08979 ID O08979 PRELIMINARY; PRT; 9 AA.
AC O08979;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AML1 protein (Fragment).
GN Name=AML1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Murine retrovirus induced tumor;
RX MEDLINE=97332339; PubMed=9188573;
RA Amtoft H.W., Sorensen A.B., Bareil C., Schmidt J., Luz A.,
RA Pedersen F.S.;
RT "Stability of AML1 (core) site enhancer mutations in T-lymphomas
RT induced by attenuated SL3-3 murine leukemia virus mutants.";
RL J. Virol. 71:5080-5087(1997).
DR EMBL; Y11802; CAA72496.1; -.
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 981 MW; 293E01E865A776D8 CRC64;

Query Match 32.7%; Score 18; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

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QY 1 QPNVH 5
   ||: |
Db 3 QPSGH 7

RESULT 7
Q7RGV8 PRELIMINARY; PRT; 10 AA.
AC Q7RGV8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY04238;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Koolij T.W., Perle M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feidblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -I- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABL01001270; EAA16068.1; -.
DR KW Hypothetical protein.
SQ SEQUENCE 10 AA; 1332 MW; F8601A30545B5051 CRC64;

Query Match 32.7%; Score 18; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YHAVNI 9
   ||: |
Db 2 HHYNI 7

RESULT 8
P82438 PRELIMINARY; PRT; 10 AA.
AC P82438;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 50 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -I- SUBCELLULAR LOCATION: CELL WALL.
CC -I- TISSUE SPECIFICITY: XYLEM.

DR GO; GO:0005618; C:cell wall; IEA.
KW Cell wall.
FT NON TER 10
SQ SEQUENCE 10 AA; 1126 MW; C68E32486AF77B46 CRC64;

Query Match 32.7%; Score 18; DB 2; Length 10;
Best Local Similarity 37.5%; Pred. No. 9.3e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PNYHAVNI 9
   ||: |
Db 2 PQYPXGNV 9

RESULT 9
FAR4_PANRE STANDARD; PRT; 7 AA.
AC P41875;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRFamide-like neuropeptide PF4 (KPNFIRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95232026; PubMed=7716079; DOI=10.1016/0196-9781(94)00162-Y;
RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P., Thim L.,
RA Kubiak T.M., Martin R.A., Geary F.G.;
RT "Isolation and preliminary biological characterization of
RT KPNFIRFamide, a novel FMRFamide-related peptide from the free-living
RT nematode, Panagrellus redivivus.";
RL Peptides 16:87-93(1995).
CC -I- FUNCTION: Myositive; induces a rapid concentration-dependent
CC muscle tension increase.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 7 7 Phenylalanine amide.
SQ SEQUENCE 7 AA; 921 MW; 69D40059C4576350 CRC64;

Query Match 30.9%; Score 17; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPNY 4
   ||: |
Db 1 KPNF 4

RESULT 10
LCK6_LEUMA STANDARD; PRT; 8 AA.
AC P19988;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leucokinin VI (L-VI).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794; DOI=10.1016/0742-8413(86)90077-0;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
RT myotropic peptides of Leucophaea maderae.";
```

RL Comp. Biochem. Physiol. 88C:27-30(1987).
 CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
 CC activity of cockroach prothorax (hindgut).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR FIR; JS0316; JS0316.
 KW Amidation; Direct protein sequencing; Neuropeptide;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD_RES 8 8 Glycine amide.
 FT MOD_RES 8 8 935 MW; 9D6365B1E9D5A5A6 CRC64;
 SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;
 Query Match 30.9%; Score 17; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.6e+06;
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QPNYHA 6
 Db | : : : :
 1 QSFHFS 6
 RESULT 11
 ID Q9UCR0 PRELIMINARY; PRT; 10 AA.
 AC Q9UCR0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE AUTOTAXIN (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92129337; PubMed=1733949;
 RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
 RA Schiffrin M.E., Liotta L.A.;
 RT "Identification, purification, and partial sequence analysis of
 RT autotaxin, a novel motility-stimulating protein.";
 RL J. Biol. Chem. 267:2524-2529(1992).
 DR GO; GO:0005576; C:extracellular; IDA.
 DR GO; GO:0030334; P:regulation of cell migration; IDA.
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1193 MW; 3E01FB40544B19D7 CRC64;
 Query Match 30.9%; Score 17; DB 2; Length 10;
 Best Local Similarity 25.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 PNYHAVNI 9
 Db | : : : :
 2 PPENINL 9
 RESULT 12
 ID Q7RSI4 PRELIMINARY; PRT; 10 AA.
 AC Q7RSI4;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=PY00373;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17XNI;
 RX PubMed=42368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Anguolli S.V., Suh B.B., Kooij T.W., Peretea M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,

RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
 RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABL0100104; EAA15335.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 10 AA; 1279 MW; 11EBECB04B4B4B50 CRC64;
 Query Match 30.9%; Score 17; DB 2; Length 10;
 Best Local Similarity 14.3%; Pred. No. 1.5e+04;
 Matches 1; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 4 YHAVNIV 10
 Db | : : : :
 4 YVVISVI 10
 RESULT 13
 ID Q8QE18 PRELIMINARY; PRT; 10 AA.
 AC Q8QE18;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Truncated envelope glycoprotein (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22961413; PubMed=14601597; DOI=10.1089/08922203322493139;
 RA Masharsky A.E., Klimov N.A., Kozlov A.P.;
 RT "Molecular cloning and analysis of full-length genome of HIV type 1
 RT strains prevalent in countries of the former Soviet Union.";
 RL AIDS Res. Hum. Retroviruses 19:933-939(2003).
 DR EMBL; AF413977; AAL78427.1; -.
 DR GO; GO:0019031; C:viral envelope; IEA.
 KW Envelope protein.
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1274 MW; A9FD6CCB544326D6 CRC64;
 Query Match 30.9%; Score 17; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.5e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QPNY 4
 Db | : : : :
 4 QKNY 7
 RESULT 14
 ID HV7_PIG STANDARD; PRT; 7 AA.
 AC HV7_PIG;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypothetical heptapeptide.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;

[1]
RN SEQUENCE, AND SYNTHESIS.
RP MEDLINE=81213980; PubMed=6263778;
RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
RA Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
RT "Isolation, structure and synthesis of a heptapeptide with in vitro
RT ACTH-releasing activity from porcine hypothalamus.";
RL Horm. Metab. Res. 13:228-232 (1981).
DR PIR; A01417; NYPG7.
KW Direct protein sequencing.
SQ SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;

Query Match 29.1%; Score 16; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YHA 6
DB 3 YHS 5

RESULT 15
P72081
ID P72081 PRELIMINARY; PRT; 7 AA.
AC P72081;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 3'-methylcephem hydroxylase (Fragment).
GN Name=cefF;
OS Nocardia lactamdurans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardineae; Pseudonocardaceae; Amycolatopsis.
OX NCBI_TaxID=1913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96009872; PubMed=7557411; DOI=10.1016/0378-1119(95)00308-S;
RA Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
RA Liras P.;
RT "Characterization of the cmh genes of Nocardia lactamdurans and
RT Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem
RT O-carbamoyltransferase for cephamycin biosynthesis.";
RL Gene 162:21-27 (1995).
DR EMBL; Z21682; CAA79797.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;

Query Match 29.1%; Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 HAV 7
DB 3 HAV 5

Search completed: May 19, 2005, 18:15:46
Job time : 115 secs

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Result No.	Score	Query Match	Length	DB	ID	Description	
1	55	100.0	10	5	AAO20570	Cysteine	
2	55	100.0	10	5	AB989835	Cysteine	
3	51	92.7	9	6	ABU11122	House dust	
4	37	67.3	9	6	ABU11108	House dust	
5	30	54.5	10	2	AA232324	Peptide digest	
6	28	50.9	8	4	AAE10569	Soybean protein	
7	28	50.9	9	8	AD885720	Human epithelial cells	
8	27	49.1	8	8	ADK09727	Human papilloma virus	
9	27	49.1	9	8	ADK09741	Human papilloma virus	
10	27	49.1	9	8	ADK09742	Human papilloma virus	
11	27	49.1	9	8	ADK09740	Human papilloma virus	
12	27	49.1	10	8	ADK09760	Human papilloma virus	
13	26	47.3	8	5	ABP46729	Human B-lymphocytes	
14	26	47.3	8	7	ADG97556	scFV VHC1	
15	26	47.3	9	6	ABR25375	Human can	
16	26	47.3	9	6	ABR25590	Human can	
17	26	47.3	9	6	ABR24431	Human can	
18	26	47.3	9	6	ABR25198	Human can	
19	26	47.3	10	2	AAK96521	Hepatitis A virus	
20	26	47.3	10	6	ABR24938	Human can	
21	26	47.3	10	6	ABR24674	Human can	
22	26	47.3	10	6	ABR25279	Human can	
23	26	47.3	10	6	ABR25474	Human can	
24	26	47.3	10	6	ABR25523	Human can	
25	26	47.3	10	6	ABR25760	Human can	

CC compositions of the invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPNYHAVNIV 10
Db 1 QPNYHAVNIV 10

RESULT 2

ABB98535
ID ABB98535 standard; peptide; 10 AA.

XX
AC ABB98535;

XX
DT 13-DEC-2002 (first entry)

XX
DE Cysteine protease epitope #2.

XX
KW Antiallergic; antiasthmatic; antiinflammatory; dermatological;
KW immunotherapy; allergen; allergic hypersensitivity reaction;
KW allergic asthma; allergic rhinitis; allergic atopic eczema;
KW cysteine protease.

XX
OS Dermatophagoides pteronyssinus.

XX
PN FR2822709-A1.

XX
PD 04-OCT-2002.

XX
PF 03-MAY-2001; 2001FR-00005929.

XX
PR 30-MAR-2001; 2001FR-00004370.

XX
PA (ANTI-) ANTIALIS SARL.

XX
PI Loria E, Terrasse G, Trehin Y;

XX
DR WPI; 2002-735037/80.

XX
PT Antiallergic composition, useful for preventing and treating e.g. asthma,
PT rhinitis or eczema, containing at least two of allergen, antihistamine
PT and histamine synthesis inhibitor.

XX
PS Claim 8; Page 6; 33pp; French.

XX
CC The present invention relates to an antiallergic pharmaceutical
CC composition (I) comprising a pharmaceutical carrier containing an active
CC agent combination of at least two of: an allergen; an antihistamine; and
CC a histamine synthesis inhibitor. (I) is used for treating or preventing
CC allergic hypersensitivity reactions, especially allergic asthma, allergic
CC rhinitis or allergic atopic eczema, in babies, children or adults. The
CC present sequence is a peptide fragment (epitope) of cysteine protease
CC from Dermatophagoides pteronyssinus, which was used as an allergen in the
CC invention

XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPNYHAVNIV 10
Db 1 QPNYHAVNIV 10

RESULT 3

ABU11122

ID ABU11122 standard; peptide; 9 AA.

XX
AC ABU11122;

XX
DT 05-FEB-2003 (first entry)

XX
DE House dust mite Der p1 antigen peptide #45.

XX
KW House dust mite; Der p1 antigen; human CD8 cell epitope; allergy;
KW immune response; atopic patient; CD8+ T-cell epitope; antiallergic.

XX
OS Dermatophagoides pteronyssinus.

XX
PN WO200281512-A1.

XX
PD 17-OCT-2002.

XX
PF 03-APR-2002; 2002WO-GB001534.

XX
PR 06-APR-2001; 2001GB-00008752.

XX
PA (ISIS-) ISIS INNOVATION LTD.

XX
PI Ogg G, Seneviratne S;

XX
DR WPI; 2003-058499/05.

XX
PT New peptide fragments of the Der p1 antigen of the house dust mite
PT Dermatophagoides pteronyssinus contain a human CD8+ T cell epitope and
PT are useful to treat and prevent allergy to the major house dust mite
PT allergen.

XX
PS Disclosure; Page 32; 47pp; English.

XX
CC The present invention relates to house dust mite (Dermatophagoides
CC pteronyssinus) Der p1 antigen peptides containing human CD8 cell
CC epitopes. The peptides of the invention are useful in the treatment of
CC human or animal patients, particularly to raise an immune response to the
CC Der p1 antigen. They are useful in the treatment and prevention of
CC allergies to the major house dust mite antigen, and to monitor disease
CC activity in atopic patients. ABU11078-ABU11146 represent house dust mite
CC Der p1 antigen peptides containing CD8+ T-cell epitopes

XX
SQ Sequence 9 AA;

Query Match 92.7%; Score 51; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPNYHAVNI 9

Db 1 QPNYHAVNI 9

RESULT 4

ABU11108

ID ABU11108 standard; peptide; 9 AA.

XX
AC ABU11108;

XX
DT 05-FEB-2003 (first entry)

XX
DE House dust mite Der p1 antigen peptide #31.

XX
KW House dust mite; Der p1 antigen; human CD8 cell epitope; allergy;
KW immune response; atopic patient; CD8+ T-cell epitope; antiallergic.

XX
OS Dermatophagoides pteronyssinus.

XX
PN WO200281512-A1.

XX
PD 17-OCT-2002.

XX

PF 03-APR-2002; 2002WO-GB001534.
 XX
 PR 06-APR-2001; 2001GB-00008752.
 XX
 PA (ISIS-) ISIS INNOVATION LTD.
 XX
 PI Ogg G, Seneviratne S;
 XX
 DR WPI; 2003-058499/05.
 XX
 XX New peptide fragments of the Der p1 antigen of the house dust mite
 PT Dermatophagoides pteronyssinus contain a human CD8+ T cell epitope and
 PT are useful to treat and prevent allergy to the major house dust mite
 PT allergen.
 XX
 PS Disclosure; Page 31; 47pp; English.
 XX
 CC The present invention relates to house dust mite (Dermatophagoides
 CC pteronyssinus) Der p1 antigen peptides containing human CD8 cell
 CC epitopes. The peptides of the invention are useful in the treatment of
 CC human or animal patients, particularly to raise an immune response to the
 CC Der p1 antigen. They are useful in the treatment and prevention of
 CC allergies to the major house dust mite antigen, and to monitor disease
 CC activity in atopic patients. ABU11078-ABU11146 represent house dust mite
 CC Der p1 antigen peptides containing CD8+ T-cell epitopes
 XX
 SQ Sequence 9 AA;
 Query Match 67.3%; Score 37; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YHAVNIV 10
 DB 1 YHAVNIV 7
 |||||
 |||||
 RESULT 5
 AAY23224
 ID AAY23224 standard; peptide; 10 AA.
 XX
 AC AAY23224;
 XX
 DT 25-AUG-1999 (first entry)
 XX
 DE Peptide derived from beta-1,2-xylosyltransferase.
 XX
 KW Beta-1,2-xylosyltransferase; beta 1,2-linked xylose; beta-linked mannose;
 KW N-linked oligosaccharide; storage glycoprotein; allergenicity; soybean.
 XX
 OS Glycine max.
 XX
 PN WO9929835-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 08-DEC-1998; 98WO-US026047.
 XX
 PR 08-DEC-1997; 97US-0067932P.
 PR 05-JAN-1998; 98US-0070418P.
 XX
 XX (UYAR-) UNIV ARKANSAS.
 XX
 PI Elbein AD, Bannon GA;
 XX
 DR WPI; 1999-385597/32.
 XX
 XX A Soybean-derived xylosyltransferase.
 PT
 PS Claim 3; Fig 4; 58pp; English.
 XX
 CC AAY23220-24 represent peptides released by beta-1,2-xylosyltransferase by
 CC Endo lys C digestion. The specification describes a plant-derived beta

CC 1,2-xylosyltransferase, where the enzyme adds a beta 1,2-linked xylose to
 CC the beta -linked mannose on the N-linked oligosaccharides of storage
 CC glycoproteins. Xylose units on N-linked oligosaccharides may play a
 CC critical role in allergenicity of plant derived glycoproteins and may
 CC also be important in regulating the structure of the oligosaccharide
 CC chains and the targeting of these proteins. Purification of a
 CC xylosyltransferase is useful in order to study its properties and
 CC specificities in the absence of interfering activities and possible
 CC inhibitors. The antibody can be used to determine the localization of the
 CC xylosyltransferase in suspension culture soybean cells and the
 CC distribution and level of the enzyme in plants as well as its levels at
 CC various stages of growth
 XX
 SQ Sequence 10 AA;
 Query Match 54.5%; Score 30; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 34;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YHAVNI 9
 DB 4 YHAINL 9
 |||||
 |||||
 RESULT 6
 AAE10569
 ID AAE10569 standard; peptide; 8 AA.
 XX
 AC AAE10569;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Soybean peptide 3 to analyse A. thaliana beta 1,2-xylosyltransferase.
 XX
 KW Beta 1,2-xylosyltransferase; transgenic plant; medicament; glycoprotein;
 KW soybean.
 XX
 OS Glycine max.
 XX
 PN WO200164901-A1.
 XX
 PD 07-SEP-2001.
 XX
 PF 02-MAR-2001; 2001WO-EP002352.
 XX
 PR 03-MAR-2000; 2000AT-00000355.
 XX
 XX (GLOE/) GLOESSL J.
 XX
 PI Gloessel J, Strasser R, Mucha J, Mach L, Altmann F, Wilson IB;
 PI Steinkellner H;
 XX
 DR WPI; 2001-582160/65.
 XX
 XX Novel DNA molecule encoding beta 1,2-xylosyltransferase, useful for
 PT producing transgenic plants and plant cells with increased efficiency in
 PT producing glycoproteins.
 XX
 XX Example 1; Fig 1; 62pp; English.
 PS
 XX The invention relates to Arabidopsis thaliana beta 1,2-xylosyltransferase
 CC plant protein and its cDNA molecule. Beta 1,2-xylosyltransferase protein
 CC nucleic acid (PNA) molecule is useful for producing transgenic plants and
 CC plant cells with increased efficiency in producing glycoproteins. The
 CC invention also relates to a method for producing recombinant human
 CC glycoproteins which is suitable for medical use. Beta 1,2-
 CC xylosyltransferase DNA is useful for immobilisation on DNA microarrays,
 CC e.g. for finding homologous sequences or for expression studies in plants
 CC or non-vertebrate animals. The invention is also useful for inactivation,
 CC suppression or over expression and production of beta 1,2-
 CC xylosyltransferase. The present sequence is soybean peptide 3 which is
 CC used for analysing Arabidopsis thaliana beta 1,2-xylosyltransferase
 XX

SQ Sequence 8 AA;

Query Match 50.9%; Score 28; DB 4; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YHAVN 8
 |||:|
 Db 4 YHAIN 8

RESULT 7
 ADE85720
 ID ADE85720 standard; peptide; 9 AA.
 AC ADE85720;
 DT 12-FEB-2004 (first entry)
 DE Human EphA2 antibody Eph099B-233.152 VH CDR3 SEQ ID NO:24.
 KW cancer; hyperproliferative cell disease; EphA2 antibody;
 KW EphA2 agonistic antibody; cytostatic; antiasthmatic; antiproliferative;
 KW antiinflammatory; vasotropic; respiratory; gene therapy;
 KW metastatic cancer; asthma; psoriasis; inflammatory bowel disease;
 KW smooth muscle restenosis; endothelial restenosis; Crohn's disease;
 KW chronic obstructive pulmonary disease; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003094859-A2.
 XX
 PD 20-NOV-2003.
 XX
 PF 12-MAY-2003; 2003WO-US015044.
 XX
 PR 10-MAY-2002; 2002US-0379322P.
 PR 14-OCT-2002; 2002US-0418213P.
 PR 03-APR-2003; 2003US-0460507P.
 XX
 PA (MEDI-) MEDIMUNE INC.
 XX
 PI Kinch MS, Carles-Kinch K, Kiener P, Langermann S;
 DR WPI: 2004-012002/01.
 DR N-PSDB; ADE85728.
 XX
 PT Treating cancer or a non-cancer hyperproliferative cell disease (e.g.
 PT asthma, psoriasis, inflammatory bowel disease or restenosis) in a patient
 PT comprises administering to the patient a therapeutic amount of an EphA2
 PT antibody.
 XX
 PS Claim 54; SEQ ID NO 24; 173pp; English.

The present invention describes a method for treating cancer or a non-cancer hyperproliferative cell disease or disorder in a patient, which comprises administering to the patient a therapeutic amount of an EphA2 antibody (I) that is an EphA2 agonistic antibody, an EphA2 cancer cell phenotype inhibiting antibody, an exposed EphA2 epitope antibody, or an antibody that binds EphA2 with a K-off of less than 3 x 10⁻³ s⁻¹. Also described: (1) a pharmaceutical composition comprising a therapeutic amount of (1) and a pharmaceutical carrier; (2) a cell line that produces (1); (3) a hybridoma deposited with the ATCC accession number PTA-4572, PTA-4573 or PTA-4574; (4) an isolated nucleic acid comprising a nucleotide sequence encoding a light chain variable domain or a heavy chain variable domain of the EphA2 antibody; (5) a vector comprising the nucleic acid described above; (6) a host cell comprising the vector; (7) methods of identifying the EphA2 agonistic antibody or the EphA2 antibody that inhibits a cancer cell phenotype, that kills cancer cells having a cancer cell phenotype or that preferentially binds an EphA2 epitope exposed on cancer cells; and (8) a method of diagnosing, prognosing or monitoring the efficacy of therapy for cancer in a patient known to or suspected to have cancer. (I) has cytostatic, antiasthmatic,

CC antiproliferative, antiinflammatory, vasotropic and respiratory activities, and can be used in gene therapy. The composition and methods are useful in managing, diagnosing, preventing or treating hyperproliferative cell diseases (i.e. metastatic cancer) or non-cancer hyperproliferative cell diseases or disorders, such as asthma, psoriasis, inflammatory bowel disease, smooth muscle restenosis, endothelial restenosis, Crohn's disease or chronic obstructive pulmonary disease. They may also be used for monitoring the efficacy of therapy for cancer in a patient known to or suspected to have cancer, and in screening for anti-cancer drugs. The present sequence is used in the exemplification of the present invention.

XX
 SQ Sequence 9 AA;

Query Match 50.9%; Score 28; DB 8; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PNYHAVN 8
 |||:|
 Db 2 PRYHAMD 8

RESULT 8
 ADK09727
 ID ADK09727 standard; peptide; 8 AA.
 AC ADK09727;
 XX
 DT 06-MAY-2004 (first entry)
 DE Human papillomavirus peptide #1782.
 XX
 KW pathogenic virus; alternative reading frame; antigenic determinant;
 KW virucide; vaccine; therapeutic agent; infection; HPV.
 XX
 OS Human papillomavirus.
 XX
 PN WO2004011650-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 24-JUL-2003; 2003WO-EP008112.
 XX
 PR 24-JUL-2002; 2002AT-00001124.
 PR 11-JUL-2003; 2003EP-00450171.
 XX
 PA (INTE-) INTERCELL AG.
 XX
 PI Mattner F, Schmidt W, Habel A;
 DR WPI: 2004-169243/16.
 XX
 PT New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
 XX
 PS Claim 18; Page 193; 220pp; English.

This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the invention.

XX
 SQ Sequence 8 AA;

Query Match 49.1%; Score 27; DB 8; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;

```

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPNYH 5
Db 2 QPRYH 6

RESULT 9
ADK09741
ID ADK09741 standard; peptide; 9 AA.
AC ADK09741;
XX
XX
DT 06-MAY-2004 (first entry)
DE Human papillomavirus peptide #1796.
DE pathogenic virus; alternative reading frame; antigenic determinant;
KW virucide; vaccine; therapeutic agent; infection; HPV.
XX
OS Human papillomavirus.
XX
PN WO2004011650-A2.
XX
PD 05-FEB-2004.
XX
PF 24-JUL-2003; 2003WO-EP008112.
XX
XX
DT 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX
XX
PA (INTE-) INTERCELL AG.
XX
PI Mattner F, Schmidt W, Habel A;
XX
DR WPI; 2004-169243/16.
XX
XX
PN WO2004011650-A2.
XX
PD 05-FEB-2004.
XX
PF 24-JUL-2003; 2003WO-EP008112.
XX
XX
PR 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX
XX
PA (INTE-) INTERCELL AG.
XX
PI Mattner F, Schmidt W, Habel A;
XX
XX
DR WPI; 2004-169243/16.
XX
XX
PT New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX
PS Claim 18; Page 193; 220pp; English.
XX
CC This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC invention.
XX
SQ Sequence 9 AA;

Query Match 49.1%; Score 27; DB 8; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPNYH 5
Db 2 QPRYH 6

RESULT 10
ADK09742
ID ADK09742 standard; peptide; 9 AA.
AC ADK09742;
XX
XX
DT 06-MAY-2004 (first entry)
DE Human papillomavirus peptide #1796.
DE pathogenic virus; alternative reading frame; antigenic determinant;
KW virucide; vaccine; therapeutic agent; infection; HPV.
XX
OS Human papillomavirus.
XX
PN WO2004011650-A2.
XX
PD 05-FEB-2004.
XX
PF 24-JUL-2003; 2003WO-EP008112.
XX
XX
DT 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX
XX
PA (INTE-) INTERCELL AG.
XX
PI Mattner F, Schmidt W, Habel A;
XX
XX
DR WPI; 2004-169243/16.
XX
XX
PT New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX
PS Claim 18; Page 193; 220pp; English.
XX
CC This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC invention.
XX
SQ Sequence 9 AA;

Query Match 49.1%; Score 27; DB 8; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPNYH 5
Db 2 QPRYH 6

RESULT 11
ADK09740
ID ADK09740 standard; peptide; 9 AA.
AC ADK09740;
XX
XX
DT 06-MAY-2004 (first entry)
DE Human papillomavirus peptide #1795.
DE pathogenic virus; alternative reading frame; antigenic determinant;
KW virucide; vaccine; therapeutic agent; infection; HPV.
XX
OS Human papillomavirus.
XX
PN WO2004011650-A2.
XX
PD 05-FEB-2004.
XX
PF 24-JUL-2003; 2003WO-EP008112.
XX
XX
DT 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX
XX
PA (INTE-) INTERCELL AG.
XX
PI Mattner F, Schmidt W, Habel A;
XX
XX
DR WPI; 2004-169243/16.
XX
XX
PT New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX
PS Claim 18; Page 193; 220pp; English.
XX
CC This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC invention.
XX
SQ Sequence 9 AA;

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XX (INTE-) INTERCELL AG.
XX Mattner F, Schmidt W, Habel A;
XX WPI; 2004-169243/16.
XX New polypeptide encoded by an alternative reading frame of a pathogenic
XX virus comprising an antigenic determinant, useful for treating or
XX preventing an infection with the pathogenic virus.
XX Claim 18; Page 193; 220pp; English.
XX This invention relates to a novel polypeptide encoded by an alternative
XX reading frame of a pathogenic virus, where the polypeptide starts with a
XX methionine amino acid residue, which comprises an antigenic determinant
XX and more than 7 amino acid residues. The invention may be useful for the
XX production of compounds with a virucide activity or the development of a
XX vaccine. The polypeptide or its fragments may be useful as a therapeutic
XX agent. It is also useful for the manufacture of a medicament for treating
XX or preventing an infection with the pathogenic virus. The present
XX sequence is that of a human papillomavirus (HPV) epitope peptide of the
XX invention.
XX Query Match 49.1%; Score 27; DB 8; Length 9;
XX Best Local Similarity 80.0%; Pred. No. 1.8e+06;
XX Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 QPNYH 5
XX 4 QPRYH 8
XX
XX RESULT 12
XX ADK09760
XX ID ADK09760 standard; peptide; 10 AA.
XX AC ADK09760;
XX
XX 06-MAY-2004 (first entry)
XX Human papillomavirus peptide #1815.
XX pathogenic virus; alternative reading frame; antigenic determinant;
XX virucide; vaccine; therapeutic agent; infection; HPV.
XX Human papillomavirus.
XX WO2004011650-A2.
XX
XX 05-FEB-2004.
XX
XX 24-JUL-2003; 2003WO-EP008112.
XX
XX 24-JUL-2002; 2002AT-00001124.
XX 11-JUL-2003; 2003EP-00450171.
XX (INTE-) INTERCELL AG.
XX Mattner F, Schmidt W, Habel A;
XX WPI; 2004-169243/16.
XX New polypeptide encoded by an alternative reading frame of a pathogenic
XX virus comprising an antigenic determinant, useful for treating or
XX preventing an infection with the pathogenic virus.
XX Claim 18; Page 193; 220pp; English.
XX This invention relates to a novel polypeptide encoded by an alternative
XX reading frame of a pathogenic virus, where the polypeptide starts with a
XX methionine amino acid residue, which comprises an antigenic determinant
XX and more than 7 amino acid residues. The invention may be useful for the
XX production of compounds with a virucide activity or the development of a
XX vaccine. The polypeptide or its fragments may be useful as a therapeutic
XX agent. It is also useful for the manufacture of a medicament for treating
XX or preventing an infection with the pathogenic virus. The present
XX sequence is that of a human papillomavirus (HPV) epitope peptide of the
XX invention.
XX Query Match 49.1%; Score 27; DB 8; Length 9;
XX Best Local Similarity 80.0%; Pred. No. 1.8e+06;
XX Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 QPNYH 5
XX 4 QPRYH 8
XX
XX RESULT 13
XX ABP46729
XX ID ABP46729 standard; peptide; 8 AA.
XX AC ABP46729;
XX
XX 19-AUG-2002 (first entry)
XX Human BlyS binding scFv VH CDR3 SEQ ID 2740.
XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX Homo sapiens.
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240816P.
XX 16-MAR-2001; 2001US-0276248P.
XX 21-MAR-2001; 2001US-0277379P.
XX 25-MAY-2001; 2001US-0293499P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX Claim 2; Page 3042; 3148pp; English.
XX This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of BlyS. The antibodies bind to BlyS
XX and so may be used to detect and quantitate the presence of BlyS in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of BlyS. They may also be

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CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

XX Sequence 8 AA;

Query Match 47.3%; Score 26; DB 5; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.8e+06;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PNYHAVNI 9
 Db 1 PSYHYMDV 8

RESULT 14
 ADG97556

ID ADG97556 standard; peptide; 8 AA.

XX AC ADG97556;

XX DT 11-MAR-2004 (first entry)

XX DE scFV VHCDR3 peptide that immunospecifically binds BlyS SeqID 2740.

XX KW antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antiasthmatic; antiarthritic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX OS Unidentified.

XX PN W02003055979-A2.

XX PD 10-JUL-2003.

XX PF 14-NOV-2002; 2002WO-US036496.

XX PR 16-NOV-2001; 2001US-0331469P.

XX PR 19-DEC-2001; 2001US-0340817P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX PS WPI; 2003-505530/47.

XX PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (BlyS), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukaemia.

XX PS Example 1; SEQ ID NO 2740; 394pp; English.

XX CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey BlyS. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of BlyS or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and

CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
 CC peptide sequence is a single chain antibody variable heavy CDR3 peptide
 CC that immunospecifically binds BlyS of the invention.

XX Sequence 8 AA;

Query Match 47.3%; Score 26; DB 7; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.8e+06;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PNYHAVNI 9
 Db 1 PSYHYMDV 8

RESULT 15

ABR25375
 ID ABR25375 standard; peptide; 9 AA.

XX AC ABR25375;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 185P3C3 HLA peptide #1010.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN W0200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US011654.

XX PR 10-APR-2001; 2001US-0282739P.

XX PR 10-APR-2001; 2001US-0283112P.

XX PR 25-APR-2001; 2001US-0286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;

XX PS WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.

XX PS Claim 13; Page 380; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

XX Sequence 9 AA;

Query Match 47.3%; Score 26; DB 6; Length 9;
 Best Local Similarity 37.5%; Pred. No. 1.8e+06;

Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 BNYHAVNI 9

Db 2 PDFHSENL 9

Search completed: May 19, 2005, 17:59:10
Job time : 146 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:59:41 ; Search time 89.5 Seconds
(without alignments)
37.375 Million cell updates/sec

Title: US-09-867-159A-4

Perfect score: 55

Sequence: 1 QPNYHAVNIV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 185062

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	10	US-09-867-159A-4
2	30	54.5	10	9	US-09-748-578-5
3	30	54.5	10	14	US-10-411-905-5
4	28	50.9	8	16	US-10-220-467A-2
5	28	50.9	8	15	US-10-436-782-24
6	26	47.3	8	10	US-09-880-748-2740
7	26	47.3	8	15	US-10-293-418-2740
8	26	47.3	10	9	US-09-851-138-204
9	25	45.5	8	10	US-09-988-493-162
10	25	45.5	8	13	US-10-007-363-4
11	25	45.5	8	16	US-10-807-553-4
12	25	45.5	9	17	US-10-820-467-236
13	24	43.6	6	17	US-10-699-114-742

14	24	43.6	6	17	US-10-699-114-959	Sequence 959, App
15	24	43.6	6	17	US-10-806-924-11	Sequence 11, Appl
16	24	43.6	6	17	US-10-806-924-705	Sequence 705, App
17	24	43.6	7	14	US-10-052-578-164	Sequence 164, App
18	24	43.6	7	14	US-10-052-578-210	Sequence 210, App
19	24	43.6	7	14	US-10-053-520-164	Sequence 164, App
20	24	43.6	7	14	US-10-053-520-210	Sequence 210, App
21	24	43.6	7	14	US-10-053-4988-164	Sequence 164, App
22	24	43.6	7	14	US-10-053-4988-210	Sequence 210, App
23	24	43.6	7	15	US-10-258-146A-22	Sequence 22, Appl
24	24	43.6	7	15	US-10-258-146A-68	Sequence 68, Appl
25	24	43.6	7	15	US-10-328-953-167	Sequence 167, App
26	24	43.6	7	15	US-10-328-953-213	Sequence 213, App
27	24	43.6	7	16	US-10-258-144-57	Sequence 57, Appl
28	24	43.6	7	16	US-10-258-144-103	Sequence 103, App
29	24	43.6	9	9	US-09-826-177-56	Sequence 56, Appl
30	24	43.6	9	15	US-10-428-335-142	Sequence 142, App
31	23	41.8	6	17	US-10-699-114-760	Sequence 760, App
32	23	41.8	6	17	US-10-699-114-1053	Sequence 1053, App
33	23	41.8	6	17	US-10-806-924-105	Sequence 105, App
34	23	41.8	6	17	US-10-806-924-723	Sequence 723, App
35	23	41.8	7	15	US-10-285-394-289	Sequence 289, App
36	23	41.8	7	15	US-10-601-837-176	Sequence 176, App
37	23	41.8	9	9	US-09-826-177-40	Sequence 40, Appl
38	23	41.8	9	9	US-09-826-177-72	Sequence 72, Appl
39	23	41.8	9	9	US-09-826-177-74	Sequence 74, Appl
40	23	41.8	9	9	US-09-826-177-84	Sequence 84, Appl
41	23	41.8	9	14	US-10-254-446A-109	Sequence 109, App
42	23	41.8	9	16	US-10-415-014-106	Sequence 106, App
43	23	41.8	9	16	US-10-415-014-219	Sequence 219, App
44	23	41.8	9	16	US-10-415-014-414	Sequence 414, App
45	23	41.8	9	16	US-10-415-014-414	Sequence 414, App

ALIGNMENTS

RESULT 1

US-09-867-159A-4
; Sequence 4, Application US/09867159A
; Publication No. US20030104013A1
; GENERAL INFORMATION:
; APPLICANT: ANTIALIS TERRASSE, GAETAN LORIA, EMILE TREHIN, YVES
; TITLE OF INVENTION: Anti-allergic pharmaceutical composition containing at least one
; FILE REFERENCE: B112812US-antialis and at least one anti-histamine compound
; CURRENT APPLICATION NUMBER: US/09/867,159A
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: FR01/04370
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: FR01/05929
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(10)
; OTHER INFORMATION: Comprises epitope from cystine protease.
US-09-867-159A-4

Query Match 100.0%; Score 55; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPNYHAVNIV 10
|||||

Db 1 QPNYHAVNIV 10
|||||

```
RESULT 2
US-09-748-578-5
; Sequence 5, Application US/09748578
; Patent No. US20010016344A1
; GENERAL INFORMATION:
; APPLICANT: Elbein, Alan D.
; APPLICANT: Bannion, Gary A.
; TITLE OF INVENTION: Purified (1,2-Xylosyltransferase and Uses Thereof
; FILE REFERENCE: D6063/D
; CURRENT APPLICATION NUMBER: US/09/748,578
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/207,223
; PRIOR FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: soybean
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a peptide released by Endo
; OTHER INFORMATION: lys C digestion of purified xylosyltransferase.
US-09-748-578-5
Query Match 54.5%; Score 30; DB 9; Length 10;
Best Local Similarity 66.7%; Pred. No. 60;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YHAVNI 9
DB 4 YHAINL 9

RESULT 3
US-10-411-905-5
; Sequence 5, Application US/10411905
; Publication No. US20030166012A1
; GENERAL INFORMATION:
; APPLICANT: Elbein, Alan D.
; APPLICANT: Bannion, Gary A.
; TITLE OF INVENTION: Purified (1,2-Xylosyltransferase and Uses Thereof
; FILE REFERENCE: D6063/D2
; CURRENT APPLICATION NUMBER: US/10/411,905
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 09/748,578
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: soybean
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a peptide released
; OTHER INFORMATION: by Endo lys C digestion of purified
; OTHER INFORMATION: xylosyltransferase.
US-10-411-905-5
Query Match 54.5%; Score 30; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 60;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YHAVNI 9
DB 4 YHAINL 9

RESULT 4
US-10-220-467A-2
; Sequence 2, Application US/10220467A
; Publication No. US20040121325A1
; GENERAL INFORMATION:
; APPLICANT: Glossl Prof., Josef
; TITLE OF INVENTION: Beta 1, 2-Xylosyltransferase-Gene from Arabidopsis
; FILE REFERENCE: SONN:019US
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; CURRENT APPLICATION NUMBER: US/10/220,467A
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: A 355/2000
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: soybean
US-10-220-467A-2
Query Match 50.9%; Score 28; DB 16; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YHAVN 8
DB 4 YHAIN 8

RESULT 5
US-10-436-782-24
; Sequence 24, Application US/10436782
; Publication No. US20040028685A1
; GENERAL INFORMATION:
; APPLICANT: Kinch, Michael
; APPLICANT: Carles-Kinch, Kelly
; APPLICANT: Kiener, Peter
; APPLICANT: Langermann, Solomon
; TITLE OF INVENTION: EphA2 Monoclonal Antibodies and Methods of Use Thereof
; FILE REFERENCE: 10271-097
; CURRENT APPLICATION NUMBER: US/10/436,782
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,322
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/418,213
; PRIOR FILING DATE: 2002-10-14
; PRIOR APPLICATION NUMBER: 60/418,213
; PRIOR FILING DATE: 2003-04-03
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-436-782-24
Query Match 50.9%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PNYHAVN 8
DB 2 PRYHAMD 8

RESULT 6
US-09-880-748-2740
; Sequence 2740, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
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; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2740
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2740

Query Match 47.3%; Score 26; DB 10; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.3e+06;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PNYHAVNI 9
|:|:|:
Db 1 PSYHYMDV 8

RESULT 7

US-10-293-418-2740
; Sequence 2740, Application US/10293418
; Publication No. US2003023996A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys

; FILE REFERENCE: PF523P2

; CURRENT APPLICATION NUMBER: US/10/293,418

; CURRENT FILING DATE: 2002-11-27

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 05/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-16

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 2740

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-293-418-2740

Query Match 47.3%; Score 26; DB 15; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.3e+06;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PNYHAVNI 9
|:|:|:
Db 1 PSYHYMDV 8

RESULT 8

US-09-851-138-204
; Sequence 204, Application US/09851138
; Publication No. US20020183508A1

; GENERAL INFORMATION:

; APPLICANT: MAERTENS, GEERT

; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES

; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC

; AGENTS

; ORGANISM: Homo sapien

; US-09-988-493-162

; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,138
; FILING DATE: 09-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,075
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; INFORMATION FOR SEQ ID NO: 204:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 204:
US-09-851-138-204

Query Match 47.3%; Score 26; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QPNYHAYV 7
|:|:|:
Db 1 RPKYHGV 7

RESULT 9

US-09-988-493-162
; Sequence 162, Application US/09988493
; Publication No. US2003006419A1

; GENERAL INFORMATION:

; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri

; APPLICANT: O'Hare, Michael John

; APPLICANT: Page, Martin John

; APPLICANT: Parekh, Rajesh Bhikhu

; TITLE OF INVENTION: Proteins, Genes, and Their Use for

; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer

; FILE REFERENCE: 2543-1-024

; CURRENT APPLICATION NUMBER: US/09/988,493

; CURRENT FILING DATE: 2002-05-21

; PRIOR APPLICATION NUMBER: PCT/GB01/01219

; PRIOR FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: GB 0006695.1

; PRIOR FILING DATE: 2000-03-20

; PRIOR APPLICATION NUMBER: GB 0007265.2

; PRIOR FILING DATE: 2000-02-24

; NUMBER OF SEQ ID NOS: 308

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 162

; LENGTH: 8

; TYPE: PRT

; ORGANISM: homo sapien

; US-09-988-493-162

Query Match 45.5%; Score 25; DB 10; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 NYHAV 7
|:|:|
Db 2 NFHAV 6

RESULT 10
US-10-007-363-4
; Sequence 4, Application US/10007363
; Publication No. US20020168354A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
; TITLE OF INVENTION: Ischemia
; FILE REFERENCE: 58600-8209 US00
; CURRENT APPLICATION NUMBER: US/10/007,363
; CURRENT FILING DATE: 2002-11-09
; PRIOR APPLICATION NUMBER: US 60/247,830
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: scrambled pseudo-epsilon RACK octapeptide
US-10-007-363-4

Query Match 45.5%; Score 25; DB 13; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PNYHAVNI 9
|:|:|
Db 1 PDYHDAGI 8

RESULT 11
US-10-807-553-4
; Sequence 4, Application US/10807553
; Publication No. US20040186055A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
; TITLE OF INVENTION: Ischemia
; FILE REFERENCE: 58600-8209 US00
; CURRENT APPLICATION NUMBER: US/10/807,553
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US/10/007,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/247,830
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: scrambled pseudo-epsilon RACK octapeptide
US-10-807-553-4

Query Match 45.5%; Score 25; DB 16; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PNYHAVNI 9
|:|:|
Db 1 PDYHDAGI 8

RESULT 12
US-10-820-467-236
; Sequence 236, Application US/10820467
; Publication No. US20050054053A1
; GENERAL INFORMATION:
; APPLICANT: Aguinaldo, Anna Marie
; APPLICANT: Beyna, Amelia Joy
; APPLICANT: Cho, Ho Sung
; APPLICANT: Desjarlais, John Rudolph
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Muchhal, Umesh
; APPLICANT: Villegas, Michael Francis Aquino
; APPLICANT: Zhukovsky, Eugene
; APPLICANT: Quesenberry, Michael Stephen
; TITLE OF INVENTION: INTERFERON VARIANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: A-71431-4
; CURRENT APPLICATION NUMBER: US/10/820,467
; CURRENT FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US 60/477,246
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/415,541
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/489,725
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US 10/676,705
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 236
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-820-467-236

Query Match 45.5%; Score 25; DB 17; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 NYHAVN 8
|:|:|
Db 3 NFHYVN 8

RESULT 13
US-10-699-114-742
; Sequence 742, Application US/10699114
; Publication No. US20050042623A1
; GENERAL INFORMATION:
; APPLICANT: Dana Ault-Riche
; APPLICANT: Bruce Atkinson
; APPLICANT: Krishnanand Kumble
; APPLICANT: Lynne Jersaltis
; APPLICANT: Gizette Sperinde
; TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND METH
; TITLE OF INVENTION: USING THE SYSTEMS
; FILE REFERENCE: 25885-1759
; CURRENT APPLICATION NUMBER: US/10/699,114
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 60/423,018
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/422,923
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 1094
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 742
; LENGTH: 6

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-699-114-742

Query Match      43.6%; Score 24; DB 17; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 QPNYH 5
Db      2 EPGYH 6

RESULT 14
US-10-699-114-959
; Sequence 959, Application US/10699114
; Publication No. US20050042623A1
; GENERAL INFORMATION:
; APPLICANT: Dana Ault-Riche
; APPLICANT: Bruce Atkinson
; APPLICANT: Krishnanand Kumble
; APPLICANT: Lynne Jersaitis
; APPLICANT: Gizette Sperinde
; TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND METHODS
; FILE REFERENCE: 25885-1759
; CURRENT APPLICATION NUMBER: US/10/699,114
; CURRENT FILING DATE: 2003-10-30
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/423,018
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/422,923
; NUMBER OF SEQ ID NOS: 1094
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 959
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-699-114-959

Query Match      43.6%; Score 24; DB 17; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 QPNYH 5
Db      1 EPGYH 5

RESULT 15
US-10-806-924-11
; Sequence 11, Application US/10806924
; Publication No. US20050095648A1
; GENERAL INFORMATION:
; APPLICANT: Geysen, H. Mario
; APPLICANT: Ault-Riche, Dana
; TITLE OF INVENTION: Method for designing linear epitopes and algorithm therefor
; FILE REFERENCE: 25885-1760
; CURRENT APPLICATION NUMBER: US/10/806,924
; CURRENT FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 911
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
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US-10-806-924-11

Query Match 43.6%; Score 24; DB 17; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPNYH 5
Db 1 EPGYH 5

Search completed: May 19, 2005, 18:19:59
Job time : 90.5 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 17:53:34 ; Search time 29.5 Seconds
(without alignments)
25.305 Million cell updates/sec

Title: US-09-867-159A-4
Perfect score: 55
Sequence: 1 QPNYHAVNIV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 115750

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	54.5	10	3	US-09-207-223-5
2	30	54.5	10	4	US-09-748-578-5
3	26	47.3	10	3	US-08-836-075A-204
4	25	45.5	9	1	US-08-615-181-108
5	25	45.5	10	1	US-08-212-433A-33
6	25	45.5	10	3	US-08-716-256-33
7	25	45.5	10	5	PCT-US95-03239-33
8	25	45.5	10	6	5436320-3
9	25	45.5	10	6	5436320-3
10	23	41.8	6	4	US-08-877-605-181
11	23	41.8	6	4	US-08-877-605-220
12	22	40.0	4	4	US-09-057-363C-18
13	22	40.0	4	1	US-08-265-107-18
14	22	40.0	7	1	US-08-092-110A-3
15	22	40.0	7	1	US-08-273-474-3
16	22	40.0	7	3	US-08-405-647B-14
17	22	40.0	7	3	US-08-935-100-3
18	22	40.0	7	3	US-09-147-933-22
19	22	40.0	7	3	US-08-985-499-14
20	22	40.0	7	5	PCT-US94-07881-3
21	22	40.0	7	5	PCT-US96-03180-14
22	22	40.0	8	3	US-08-947-965-62
23	22	40.0	8	3	US-08-444-818-404
24	22	40.0	9	2	US-08-318-856A-34
25	22	40.0	10	3	US-08-836-075A-195
26	21	38.2	4	1	US-08-456-424-79
27	21	38.2	4	1	US-08-456-424-80

28	21	38.2	5	2	US-08-558-823-12	Sequence 12, Appl
29	21	38.2	5	3	US-08-604-991-14	Sequence 14, Appl
30	21	38.2	5	3	US-09-363-639-14	Sequence 14, Appl
31	21	38.2	6	2	US-08-428-131-3	Sequence 3, Appli
32	21	38.2	6	2	US-08-558-823-15	Sequence 15, Appl
33	21	38.2	6	2	US-08-558-823-16	Sequence 16, Appl
34	21	38.2	6	2	US-08-310-912A-104	Sequence 104, App
35	21	38.2	6	3	US-08-893-534A-44	Sequence 44, Appl
36	21	38.2	6	3	US-08-841-089-104	Sequence 104, App
37	21	38.2	6	3	US-09-078-596-3	Sequence 3, Appli
38	21	38.2	6	3	US-08-939-853A-28	Sequence 28, Appl
39	21	38.2	6	3	US-08-996-679-44	Sequence 44, Appl
40	21	38.2	6	3	US-09-115-395-19	Sequence 19, Appl
41	21	38.2	6	3	US-09-301-085-104	Sequence 104, App
42	21	38.2	6	3	US-09-507-102-44	Sequence 44, Appl
43	21	38.2	6	3	US-09-250-059-34	Sequence 34, Appl
44	21	38.2	6	3	US-09-248-074-34	Sequence 34, Appl
45	21	38.2	6	3	US-09-187-859-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1

US-09-207-223-5

; Sequence 5, Application US/09207223
; Patent No. 6168937
; GENERAL INFORMATION:
; APPLICANT: Elbein, Alan D.
; APPLICANT: Bannon, Gary A.
; TITLE OF INVENTION: Purified (1,2-Xylosyltransferase and Uses Thereof
; FILE REFERENCE: D6063
; CURRENT APPLICATION NUMBER: US/09/207,223
; CURRENT FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 60/067,932
; EARLIER FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: soybean
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a peptide released by Endo lys C
; OTHER INFORMATION: digestion of purified xylosyltransferase.

Query Match 54.5%; Score 30; DB 3; Length 10;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YHAVNI 9
|||:
Db 4 YHAINL 9

RESULT 2

US-09-748-578-5

; Sequence 5, Application US/09748578
; Patent No. 6593462
; GENERAL INFORMATION:
; APPLICANT: Elbein, Alan D.
; APPLICANT: Bannon, Gary A.
; TITLE OF INVENTION: Purified (1,2-Xylosyltransferase and Uses Thereof
; FILE REFERENCE: D6063/D
; CURRENT APPLICATION NUMBER: US/09/748,578
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/207,223
; PRIOR FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: soybean

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/ FEATURE:
/ OTHER INFORMATION: Amino acid sequence of a peptide released by Endo
/ OTHER INFORMATION: lys C digestion of purified xylosyltransferase.
US-09-748-578-5

Query Match      54.5%; Score 30; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YHAVNI 9
Db 4 YHAINL 9

RESULT 3
US-08-836-075A-204
/ Sequence 204, Application US/08836075A
/ Patent No. 6180768
/ GENERAL INFORMATION:
/ APPLICANT: MAERTENS, GEERT
/ APPLICANT: STUYVER, LIEVEN
/ TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
/ TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
/ TITLE OF INVENTION: AGENTS
/ NUMBER OF SEQUENCES: 207
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ARNOLD, WHITE & DURKEE
/ STREET: P.O. BOX 4433
/ CITY: HOUSTON
/ STATE: TEXAS
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Microsoft Word 6.0 / ASCII text output
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/836,075A
/ FILING DATE: 21 Apr 1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP95/04155
/ FILING DATE: 23 Oct 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 94870166.9
/ FILING DATE: 21 Oct 1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 95870076.7
/ FILING DATE: 28 Jun 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KAMMERER, PATRICIA A.
/ REGISTRATION NUMBER: 29,775
/ REFERENCE/DOCKET NUMBER: INNS:004
/ INFORMATION FOR SEQ ID NO: 204:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-836-075A-204

Query Match      47.3%; Score 26; DB 3; Length 10;
Best Local Similarity 57.1%; Pred. No. 86;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QPNYHAV 7
Db 1 RPKYQV 7

RESULT 4
US-08-615-181-108
/ Sequence 108, Application US/08615181
```

```
/ Patent No. 5756666
/ GENERAL INFORMATION:
/ APPLICANT: MASAFUMI, TAKIGUCHI
/ APPLICANT: MIWA, KIYOSHI
/ TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE
/ TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND
/ TITLE OF INVENTION: CURING AIDS
/ NUMBER OF SEQUENCES: 115
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
/ ADDRESSEE: P.C.
/ STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
/ CITY: ARLINGTON
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22202
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/615,181
/ FILING DATE: 04-APR-1996
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/JP94/01756
/ FILING DATE: 19-OCT-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 261302/1993
/ FILING DATE: 19-OCT-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: OBLON, NORMAN F.
/ REGISTRATION NUMBER: 24,618
/ REFERENCE/DOCKET NUMBER: 10-796-0 PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-413-3000
/ TELEFAX: 703-413-2220
/ INFORMATION FOR SEQ ID NO: 108:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ ORIGINAL SOURCE:
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
/ US-08-615-181-108

Query Match      45.5%; Score 25; DB 1; Length 9;
Best Local Similarity 62.5%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PNYHAVNI 9
Db 2 PSGHAVGI 9

RESULT 5
US-08-212-433A-33
/ Sequence 33, Application US/08212433A
/ Patent No. 5538897
/ GENERAL INFORMATION:
/ APPLICANT: YACES, III, John R.
/ APPLICANT: Eng, James K.
/ TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
/ TITLE OF INVENTION: PATTERNS OF PEPTIDES TO IDENTIFY AMINO ACID SEQUENCES IN
/ TITLE OF INVENTION: DATABASES
/ NUMBER OF SEQUENCES: 46
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Khourie and Crew
/ STREET: One Market Plaza, Steuart St. Tower
/ CITY: San Francisco
```

STATE: CA
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212.433A
FILING DATE: 14-MAR-1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Hughes, Richard L.
REGISTRATION NUMBER: 31,264
REFERENCE/DOCKET NUMBER: 16336-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-212-433A-33

Query Match 45.5%; Score 25; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPNY 4
Db 6 QPNY 9

RESULT 6
US-08-716-256-33
Sequence 33, Application US/08716256
Patent No. 6017693
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
TITLE OF INVENTION: PATTERNS TO IDENTIFY NUCLEOTIDE, AMINO ACID OR
TITLE OF INVENTION: CARBOHYDRATE SEQUENCES IN DATABASES OR TO IDENTIFY
TITLE OF INVENTION: ORGANISMS
NUMBER OF SEQUENCES: 46
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,256
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03239
FILING DATE: 14-MAR-1995
APPLICATION NUMBER: US 08/212,433
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 16336-2PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-716-256-33

Query Match 45.5%; Score 25; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPNY 4
Db 6 QPNY 9

RESULT 7
PCT-US95-03239-33
Sequence 33, Application PC/TUS9503239
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
TITLE OF INVENTION: PATTERNS TO IDENTIFY NUCLEOTIDE, AMINO ACID OR
TITLE OF INVENTION: CARBOHYDRATE SEQUENCES IN DATABASES OR TO IDENTIFY
TITLE OF INVENTION: ORGANISMS
NUMBER OF SEQUENCES: 46
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03239
FILING DATE: 14-MAR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,433
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 16336-2PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-03239-33

Query Match 45.5%; Score 25; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPNY 4
Db 6 QPNY 9

RESULT 8
5436320-3
Patent No. 5436320
APPLICANT: SPIEGEL, ALLEN M.
TITLE OF INVENTION: ANTIBODY REAGENTS THAT IDENTIFY THE
CARBOXY-TERMINAL PEPTIDE OF THE GTP-BINDING PROTEIN G
NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,377
FILING DATE: 14-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 564,675

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/ FILING DATE: 08-AUG-1990
/ APPLICATION NUMBER: 365,919
/ FILING DATE: 15-JUN-1989
/ APPLICATION NUMBER: 100,909
/ FILING DATE: 25-SEP-1987
/ SEQ ID NO:3:
/ LENGTH: 10
5436320-3

Query Match
Best Local Similarity 45.5%; Score 25; DB 6; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPNY 4
Db 6 QPNY 9

RESULT 9
5436320-3
/ Patent No. 5436320
/ APPLICANT: SPIEGEL, ALLEN M.
/ TITLE OF INVENTION: ANTIBODY REAGENTS THAT IDENTIFY THE
/ CARBOXY-TERMINAL PEPTIDE OF THE GTP-BINDING PROTEIN G
/ NUMBER OF SEQUENCES: 10
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/820,377
/ FILING DATE: 14-JAN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 564,675
/ FILING DATE: 08-AUG-1990
/ APPLICATION NUMBER: 365,919
/ FILING DATE: 15-JUN-1989
/ APPLICATION NUMBER: 100,909
/ FILING DATE: 25-SEP-1987
/ SEQ ID NO:3:
/ LENGTH: 10
5436320-3

Query Match
Best Local Similarity 45.5%; Score 25; DB 6; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPNY 4
Db 6 QPNY 9

RESULT 10
US-08-877-605-181
/ Sequence 181, Application US/08877605
/ Patent No. 6582965
/ GENERAL INFORMATION:
/ APPLICANT: Robert Townsend
/ APPLICANT: Raj Parekh
/ APPLICANT: Sally Prime
/ APPLICANT: Nick Webb
/ TITLE OF INVENTION: A METHOD FOR DE NOVO PEPTIDE SEQUENCE DETERMINATION
/ FILE REFERENCE: 9195-004
/ CURRENT APPLICATION NUMBER: US/08/877,605
/ CURRENT FILING DATE: 1997-06-18
/ NUMBER OF SEQ ID NOS: 353
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO:181
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Peptide X Library
US-08-877-605-181

Query Match
Best Local Similarity 41.8%; Score 23; DB 4; Length 6;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NYHAV 7
Db 1 DYHAI 5

RESULT 11
US-08-877-605-220
/ Sequence 220, Application US/08877605
/ Patent No. 6582965
/ GENERAL INFORMATION:
/ APPLICANT: Robert Townsend
/ APPLICANT: Raj Parekh
/ APPLICANT: Sally Prime
/ APPLICANT: Nick Webb
/ TITLE OF INVENTION: A METHOD FOR DE NOVO PEPTIDE SEQUENCE DETERMINATION
/ FILE REFERENCE: 9195-004
/ CURRENT APPLICATION NUMBER: US/08/877,605
/ CURRENT FILING DATE: 1997-06-18
/ NUMBER OF SEQ ID NOS: 353
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO:220
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Peptide X Library
US-08-877-605-220

Query Match
Best Local Similarity 41.8%; Score 23; DB 4; Length 6;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 NYHAV 7
Db 1 DYHAI 5

RESULT 12
US-09-057-363C-18
/ Sequence 18, Application US/09057363C
/ Patent No. 6551994
/ GENERAL INFORMATION:
/ APPLICANT: Blaschuk, Orest W.
/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
/ INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN
/ NUMBER OF SEQUENCES: 73
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Seed Intellectual Property Law Group
/ STREET: 701 Fifth Avenue, Suite 6300
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/057,363C
/ FILING DATE: 08-Apr-1998
/ CLASSIFICATION: <unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Christiansen, William T.
/ REGISTRATION NUMBER: 44,614
/ REFERENCE/DOCKET NUMBER: 100086.406
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 692-6031
/ INFORMATION FOR SEQ ID NO: 18:
```



```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-057-363C-18

Query Match          40.0%; Score 22; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 HAVN 8
Db      1 HAVN 4

RESULT 13
US-09-265-107-18
; Sequence 18, Application US/09265107A
; Patent No. 6683048
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR STIMULATING
; FILE REFERENCE: 100086.406C1
; CURRENT APPLICATION NUMBER: US/09/265,107A
; CURRENT FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Linear peptide modulating agent
US-09-265-107-18

Query Match          40.0%; Score 22; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 HAVN 8
Db      1 HAVN 4

RESULT 14
US-08-092-110A-3
; Sequence 3, Application US/08092110A
; Patent No. 5585477
; GENERAL INFORMATION:
; APPLICANT: Kilpatrick, David R.
; TITLE OF INVENTION: POLIOVIRUS SPECIFIC PRIMERS AND
; METHOD OF INVENTION: METHODS OF DETECTION UTILIZING THE SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, The Candler Building, 127
; STREET: Peachtree Street, NE
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/092,110A
; FILING DATE: 13-JUL-1993

Query Match          40.0%; Score 22; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 NYHAVN 8
Db      2 NYHAVN 7

CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.075
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-092-110A-3

Query Match          40.0%; Score 22; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 NYHAVN 8
Db      2 NYHAVN 7

RESULT 15
US-08-273-474-3
; Sequence 3, Application US/08273474
; Patent No. 5691134
; GENERAL INFORMATION:
; APPLICANT: Kilpatrick, David R.
; TITLE OF INVENTION: POLIOVIRUS SPECIFIC PRIMERS AND METHODS
; METHOD OF INVENTION: OF DETECTION UTILIZING THE SAME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, The Candler Building, 127
; STREET: Peachtree Street, NE
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,474
; FILING DATE: 13-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.617
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-273-474-3

Query Match          40.0%; Score 22; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 NYHAVN 8
```

Db | | | |
2 NGHALN 7

Search completed: May 19, 2005, 18:11:53
Job time : 30.5 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: May 19, 2005, 18:16:02 ; Search time 38 Seconds
(without alignments)
22.788 Million cell updates/sec

Title: US-09-867-159A-5

Perfect score: 57

Sequence: 1 WTVRNSWDT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	45.6	9	2	PT0299
2	22	38.6	5	2	PT0580
3	22	38.6	8	2	A38887
4	19	33.3	9	2	A4244
5	18	31.6	6	2	A31263
6	17	29.8	7	2	PT0519
7	17	29.8	6	2	S33244
8	17	29.8	7	2	S33245
9	17	29.8	7	2	S33246
10	16	28.1	4	2	PT0661
11	16	28.1	6	2	A61068
12	16	28.1	7	2	PH1602
13	16	28.1	7	4	I55382
14	16	28.1	8	2	S19288
15	16	28.1	8	2	JS0315
16	16	28.1	8	2	JS0316
17	16	28.1	8	2	JS0317
18	16	28.1	9	2	A43848
19	15	26.3	6	2	B31263
20	15	26.3	7	2	PN0649
21	15	26.3	7	2	A61081
22	15	26.3	8	2	S10596
23	15	26.3	8	2	JS0318
24	15	26.3	9	2	S07205
25	15	26.3	9	2	S07204
26	15	26.3	9	2	PT0231
27	15	26.3	9	2	I58350
28	15	26.3	9	2	PC2021
29	15	26.3	9	2	D57444

30 14 24.6 5 2 PT0308 Ig heavy chain CRD
31 14 24.6 6 2 S66195 alcohol dehydrogen
32 14 24.6 9 2 A28495 conopressin G - co
33 14 24.6 9 2 B28495 conopressin S - co
34 14 24.6 9 2 S07241 litorin - Rohde's
35 14 24.6 9 2 PT0270 Ig heavy chain CRD
36 14 24.6 9 2 S39040 lysine-conopressin
37 13 22.8 5 2 PT0690 T-cell receptor be
38 13 22.8 6 2 B35640 cerebellar degener
39 13 22.8 6 2 PT0630 T-cell receptor be
40 13 22.8 6 2 PD0028 pev-kinin 2 - pena
41 13 22.8 7 2 S09066 Globulin IV alpha
42 13 22.8 8 2 B44960 neuropeptide Led-C
43 13 22.8 8 2 S08996 hypertrehalosemic
44 13 22.8 8 2 B49823 adipokinetic hormo
45 13 22.8 8 2 A59495 Vesicle associated

ALIGNMENTS

RESULT 1

PT0299

Ig heavy chain CRD3 region (clone 5-103B) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C/Accession: PT0299

R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A/Reference number: PT0222; MUID:91108337; PMID:1899102

A/Accession: PT0299

A/Molecule type: DNA

A/Residues: 1-9 <YAM>

A/Experimental source: B lymphocyte

C/Keywords: heterotetramer; immunoglobulin

Query Match 45.6%; Score 26; DB 2; Length 9;

Best Local Similarity 80.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RNSWD 8

Db 1 RESWD 5

RESULT 2

PT0580

T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C/Accession: PT0580

R/Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A/Reference number: PT0509; MUID:91277601; PMID:1711558

A/Accession: PT0580

A/Status: translation not shown

A/Molecule type: mRNA

A/Residues: 1-5 <FEE>

A/Experimental source: day 19 fetal thymus, strain BALB/c

C/Keywords: T-cell receptor

Query Match 38.6%; Score 22; DB 2; Length 5;

Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NSWD 8

Db 2 SSWD 5

RESULT 3

A38887
T-cell receptor gamma chain (St.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: A38887
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene
A:Reference number: A41946; MUID:92049316; PMID:1658619
A:Accession: A38887
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-8 <WHE>
C:Keywords: T-cell receptor

Query Match 38.6%; Score 22; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SWDT 9
|||
Db 2 SWDS 5

RESULT 4
A24244
adipokinetic hormone - bollworm
N:Alternate names: Hez-AKH
C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C:Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A24244
R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway
Biochem. Biophys. Res. Commun. 135, 622-628, 1986
A:Title: Isolation and primary structure of a peptide from the corpora cardiaca of Heliothis zea
A:Reference number: A24244; MUID:86186794; PMID:3964263
A:Accession: A24244
A:Molecule type: protein
A:Residues: 1-9 <JAF>
A:Cross-references: UNIPROT:P08901
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 33.3%; Score 19; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVRNSW 7
|||
Db 3 TFTSSW 8

RESULT 5
A31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum
C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Welles, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase gene of Plasmodium falciparum is associated with resistance to pyrimethamine
A:Reference number: A94217; MUID:89057886; PMID:2904149
A:Accession: A31263
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 31.6%; Score 18; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 SWDT 9
|||
Db 2 SWES 5

RESULT 6
PT0519
T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0519
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0519
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 29.8%; Score 17; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WD 8
|||
Db 5 WD 6

RESULT 7
S33244
neuroendocrine peptide Wamide-1 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S33244
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: Wamide-1, -2 and -3: novel neuroendocrine peptides isolated from ganglia of the giant African snail Achatina fulica
A:Reference number: S33244; MUID:93265912; PMID:8495720
A:Accession: S33244
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>
A:Cross-references: UNIPROT:P35921

Query Match 29.8%; Score 17; DB 2; Length 7;
Best Local Similarity 28.6%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WTVRNSW 7
|||
Db 1 WKEMSVW 7

RESULT 8
S33245
neuroendocrine peptide Wamide-2 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S33245
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: Wamide-1, -2 and -3: novel neuroendocrine peptides isolated from ganglia of the giant African snail Achatina fulica
A:Reference number: S33244; MUID:93265912; PMID:8495720
A:Accession: S33245
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>
A:Cross-references: UNIPROT:P35919

Query Match 29.8%; Score 17; DB 2; Length 7;

Best Local Similarity 28.6%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WTVRNSW 7
| : |
Db 1 WREMSVW 7

RESULT 9
S33246
neuromodulatory peptide Wamide-3 - giant African snail
C;Species: Achatina fullca (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S33246
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A;Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of
A;Reference number: S33244; MUID:93265912; PMID:8495720
A;Accession: S33246
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIN>
A;Cross-references: UNIPROT:P35920

Query Match 29.8%; Score 17; DB 2; Length 7;
Best Local Similarity 28.6%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WTVRNSW 7
| : |
Db 1 WKQMSVW 7

RESULT 10
PT0661
T-cell receptor beta chain V-D-J region (121-18V) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: PT0661
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0661
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <PEE>
A;Cross-references: UNIPROT:Q8BZQ7; UNIPROT:Q8CCN5
A;Experimental source: day 4 postnatal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 28.1%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WT 2
| |
Db 3 WT 4

RESULT 11
A61068
locustakinin - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A61068
R;Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.
Regul. Pept. 37, 49-57, 1992
A;Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, pri
A;Reference number: A61068; MUID:92262851; PMID:1595017
A;Accession: A61068
A;Molecule type: protein
A;Residues: 1-6 <SCH>

A;Cross-references: UNIPROT:P41491
C;Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide
P;6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.1%; Score 16; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NSW 7
| | |
Db 3 SSW 5

RESULT 12
PH1602
Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1602
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1602
A;Molecule type: DNA
A;Residues: 1-7 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 28.1%; Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WT 2
| |
Db 6 WT 7

RESULT 13
I55382
hypothetical peptide PA11 promoter region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 20-Apr-2000
C;Accession: I55382
R;Dawson, S.J.; Wiman, B.; Hamsten, A.; Green, F.; Humphries, S.; Henney, A.M.
J. Biol. Chem. 268, 10739-10745, 1993
A;Title: The two allele sequences of a common polymorphism in the promoter of the plasmi
A;Reference number: I55382; MUID:93266509; PMID:8388372
A;Accession: I55382
A;Status: translation not shown; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-7 <DAW>
A;Cross-references: GB:M91557; NID:g190020; PIDN:AAA60110.1; PID:g190021
C;Comment: This is the hypothetical translation of a sequence from the PA11 gene promote
C;Genetics:
A;Gene: GDB:PA11
A;Cross-references: GDB:I20297; OMIM:173360
A;Map position: 7q21.3-7q22

Query Match 28.1%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WT 2
| |
Db 1 WT 2

RESULT 14
S19288
acylase - Kluyvera cryocrescens
C;Species: Kluyvera cryocrescens
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C/Accession: S19288
R/Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.
Biochem. J. 280: 659-662, 1991
A/Title: Chemical modification of serine at the active site of penicillin acylase from K
A/Reference number: S19288; MUID:92109664; PMID:1764029
A/Accession: S19288
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-8 <MAP>
A/Cross-references: UNIPROT:Q7M124

Query Match 28.1%; Score 16; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 NSW 7
DB 2 NMW 4

RESULT 15
JS0315
leucokinin V - Madeira cockroach
C/Species: Leucophaea maderae (Madeira cockroach)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: JS0315
R/Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A/Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic
A/Reference number: JS0315
A/Accession: JS0315
A/Molecule type: protein
A/Residues: 1-8 <HOL>
A/Cross-references: UNIPROT:P19987
C/Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C/Keywords: amidated carboxyl end; cephalomyotropic peptide
F/8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.1%; Score 16; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 NSW 7
DB 5 SSW 7

Search completed: May 19, 2005, 19:26:29
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 18:12:01 ; Search time 173 Seconds
(without alignments)
26.640 Million cell updates/sec

Title: US-09-867-159A-5
Perfect score: 57
Sequence: 1 WTVRNSWDT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1455

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27.5	48.2	9	2	Q38366
2	25	43.9	9	2	Q9H3Y3
3	21	36.8	4	1	OCF3 OCTMI
4	21	36.8	7	2	Q8GI04
5	21	36.8	8	1	LCK1 LEUMA
6	21	36.8	8	1	LCK3 LEUMA
7	21	36.8	8	1	PK1 PERAM
8	21	36.8	8	1	PK3 PERAM
9	21	36.8	8	1	PK5 PERAM
10	21	36.8	8	2	Q8G940
11	21	36.8	9	2	Q8GL26
12	21	36.8	9	2	Q9R9C4
13	19	33.3	8	2	Q37854
14	19	33.3	8	2	Q8GL21
15	19	33.3	9	1	AKH HELZE
16	19	33.3	9	2	Q8GL31
17	18	31.6	8	1	C125_CYPDO
18	17	29.8	7	1	WWA1_ACHFU
19	17	29.8	7	1	WWA2_ACHFU
20	17	29.8	7	1	WWA3_ACHFU
21	17	29.8	7	2	O49223
22	17	29.8	8	2	O62721
23	17	29.8	8	2	P79940
24	17	29.8	9	2	Q6LDB5
25	17	29.8	9	2	Q673W5
26	17	29.8	9	2	Q673W6
27	17	29.8	9	2	Q673W7
28	17	29.8	9	2	Q673W8
29	17	29.8	9	2	Q673W9
30	17	29.8	9	2	Q673X0
31	17	29.8	9	2	Q673X1

32 17 29.8 9 2 Q673X2 pseudobias
33 17 29.8 9 2 Q673X3 prionops sc
34 17 29.8 9 2 Q673X4 prionops re
35 17 29.8 9 2 Q673X5 platyateira
36 17 29.8 9 2 Q673X6 oriolus xan
37 17 29.8 9 2 Q673X7 nilaus afer
38 17 29.8 9 2 Q673X8 bias flammu
39 17 29.8 9 2 Q673X9 malaconotus
40 17 29.8 9 2 Q673Y0 lanius coll
41 17 29.8 9 2 Q673Y1 lanioturdus
42 17 29.8 9 2 Q673Y2 laniarius 1
43 17 29.8 9 2 Q673Y3 laniarius f
44 17 29.8 9 2 Q673Y4 laniarius b
45 17 29.8 9 2 Q673Y5 laniarius a

ALIGNMENTS

RESULT 1
Q38366 PRELIMINARY; PRT; 9 AA.
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE E gene product (Fragment).
OS Bacteriophage phi-X174.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10847;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88118956; PubMed=2963134;
RA Buckley K.J., Hayashi M.;
RT "Role of premature translational termination in the regulation of
expression of the phi X174 lysis gene.";
RL J. Mol. Biol. 198:599-607(1987).
DR EMBL; X07809; CAA30668.1; -
FT NON TER 9
SQ SEQUENCE 9 AA; 1207 MW; C093B37731B36412 CRC64;

Query Match 48.2%; Score 27.5; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.6e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

Qy 1 WTVRNSWDT 9
||: |||
Db 4 WTL---WDT 9

RESULT 2
Q9H3Y3 PRELIMINARY; PRT; 9 AA.
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE DJ839811.1 (Novel protein with a Kunitz/Bovine pancreatic trypsin
inhibitor domain and WAP-type (Whey Acidic Protein) 'four-disulfide
core' domains) (Fragment).
GN Name=dj461P17.1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL121778; CAB76844.1; -
FT NON TER 9
SQ SEQUENCE 9 AA; 1036 MW; 2C417B01B412D1B3 CRC64;

Query Match 43.9%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WTVR 4
DB 2 WTVR 5

RESULT 3
OCP3_OCTMI STANDARD; PRT; 4 AA.
ID OCP3_OCTMI
AC P58639;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cardioactive peptides Ocp-3/Ocp-4.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
Octopus minor.";
RL Peptides 21:623-630 (2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
inotropic effects on the heart. Ocp-4 is a 1000 time less active
than Ocp-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- FTM: Ocp-4 has D-Ser instead of L-Ser.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGES=1-4; NOTE=Ref.1.
KW D-amino acid; Direct protein sequencing; Hormone.
FT MOD RES 2 2 D-serine (in form Ocp-4).
SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 36.8%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SWD 8
DB 2 SWD 4

RESULT 4
Q8GL04 PRELIMINARY; PRT; 7 AA.
AC Q8GL04;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PF-50 protein (Fragment).
GN Name=PF-50;
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-5.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=93-0107;
RX MEDLINE=22610300; PubMed=12724373; DOI=10.1099/mic.0.26120-0;
RA Miller J.C., Stevenson B.;
RT "Immunological and genetic characterization of Borrelia burgdorferi
Rapa and Eppa proteins.";
RL Microbiology 149:1113-1125 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=93-0107;
RX MEDLINE=22990544; PubMed=14629041;

RA Stevenson B., Miller J.C.;
RT "Intra- and interbacterial genetic exchange of Lyme disease spirochete
erp genes generates sequence identity amidst diversity.";
RL J. Mol. Evol. 57:309-324 (2003).
DR EMBL; AY142103; AAN17848.1; -.
KW Plasmid.
FT NON TER 1 1
SQ SEQUENCE 7 AA; 914 MW; 6337244330504310 CRC64;

Query Match 36.8%; Score 21; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WTVR 5
DB 1 WIKN 5

RESULT 5
LCK1_LEUMA STANDARD; PRT; 8 AA.
ID LCK1_LEUMA
AC F21140;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leucokinin I (L-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides from
Leucophaea maderae: members of a new family of Cephalomyotroptins.";
RL Comp. Biochem. Physiol. 84C:205-211 (1986).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
activity of cockroach prothodum (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 8 8 Glycine amide.
SQ SEQUENCE 8 AA; 893 MW; DC6365B449CDC76A CRC64;

Query Match 36.8%; Score 21; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NSW 7
DB 5 NSW 7

RESULT 6
LCK3_LEUMA STANDARD; PRT; 8 AA.
ID LCK3_LEUMA
AC F21142;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leucokinin III (L-III).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides from
Leucophaea maderae: members of a new family of Cephalomyotroptins.";


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RL Comp. Biochem. Physiol. 84C:271-276 (1986).
CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach prothodeum (hindgut).
CC -1- SUBCELLULAR LOCATION: Secreted.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 8 8 Glycine amide.
SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;

Query Match 36.8%; Score 21; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NSW 7
Db |||
5 NSW 7

RESULT 7
PK3_PERAM STANDARD; PRT; 8 AA.
AC P82685;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Kinin-1 (Pea-K-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Corpora cardiaca;
RX MDLINE=98010462; PubMed=9350979; DOI=10.1016/S0167-0115(97)01029-X;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gade G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205 (1997).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the kinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 8 8 Glycine amide.
SQ SEQUENCE 8 AA; 950 MW; 326365B449D5A774 CRC64;

Query Match 36.8%; Score 21; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NSW 7
Db |||
5 NSW 7

RESULT 8
PK3_PERAM STANDARD; PRT; 8 AA.
AC P82687;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Kinin-3 (Pea-K-3).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.

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RC TISSUE=Corpora cardiaca;
RX MDLINE=98010462; PubMed=9350979; DOI=10.1016/S0167-0115(97)01029-X;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gade G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205 (1997).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC NOTE=Ref.1.
CC -1- MASS SPECTROMETRY: MW=907.92; METHOD=Electrospray; RANGE=1-8;
CC -1- SIMILARITY: Belongs to the kinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 8 8 Glycine amide.
SQ SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;

Query Match 36.8%; Score 21; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NSW 7
Db |||
5 NSW 7

RESULT 9
PK5_PERAM STANDARD; PRT; 8 AA.
AC P82689;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Kinin-5 (Pea-K-5).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Corpora cardiaca;
RX MDLINE=98010462; PubMed=9350979; DOI=10.1016/S0167-0115(97)01029-X;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gade G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205 (1997).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC NOTE=Ref.1.
CC -1- MASS SPECTROMETRY: MW=864.10; METHOD=Electrospray; RANGE=1-8;
CC -1- SIMILARITY: Belongs to the kinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 8 8 Glycine amide.
SQ SEQUENCE 8 AA; 865 MW; C76365B449CDC775 CRC64;

Query Match 36.8%; Score 21; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NSW 7
Db |||
5 NSW 7

RESULT 10
Q8G940 PRELIMINARY; PRT; 8 AA.
AC Q8G940;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

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DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE PF-50 protein (Fragment).
GN Name=PF-50;
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-9, and Plasmid group cp32-12.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DN127c19-2; PLASMID=group cp32-9;
RX MEDLINE=22610300; PubMed=12724373; DOI=10.1099/mic.0.26120-0;
RA Miller J.C., Stevenson B.;
RT "Immunological and genetic characterization of Borrelia burgdorferi
  BapA and EppA proteins.";
RL Microbiology 149:1113-1125 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DN127c19-2, and Sh-2-82;
RX PLASMID=group cp32-9, and group cp32-12;
RX MEDLINE=22990544; PubMed=14629041;
RA Stevenson B., Miller J.C.;
RT "Intra- and interbacterial genetic exchange of Lyme disease spirochete
  erp genes generates sequence identity amidst diversity.";
RL J. Mol. Evol. 57:309-324 (2003).
DR EMBL; AY142104; AAN17853.1; -.
DR EMBL; AY142097; AAN17907.1; -.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 8 AA; 1042 MW; 1437244330504373 CRC64;

Query Match 36.8%; Score 21; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WTVRN 5
DB 2 WIKN 6

RESULT 11
Q8GL26 PRELIMINARY; PRT; 9 AA.
AC Q8GL26;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE PF-50 protein (Fragment).
GN Name=PF-50;
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-5.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sh-2-82;
RX MEDLINE=22990544; PubMed=14629041;
RA Stevenson B., Miller J.C.;
RT "Intra- and interbacterial genetic exchange of Lyme disease spirochete
  erp genes generates sequence identity amidst diversity.";
RL J. Mol. Evol. 57:309-324 (2003).
DR EMBL; AY142092; AAN17873.1; -.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 9 AA; 1206 MW; 5A4A244330504373 CRC64;

Query Match 36.8%; Score 21; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WTVRN 5
DB 3 WIKN 7
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RESULT 12
Q9R9C4 PRELIMINARY; PRT; 9 AA.
AC Q9R9C4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Borrelia burgdorferi plasmid cp32-2, possible partition proteins,
  complete cds (PF-50 protein) (Fragment).
GN Name=PF-50;
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid cp32-2, and plasmid group cp32-4.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B31; PLASMID=cp32-2;
RX MEDLINE=98361033; PubMed=9695920;
RA Stevenson B., Casjens S., Rosa P.;
RT "Evidence of past recombination events among the genes encoding the
  Erp antigens of Borrelia burgdorferi.";
RL Microbiology 144:1869-1879 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sh-2-82; PLASMID=group cp32-4;
RX MEDLINE=22990544; PubMed=14629041;
RA Stevenson B., Miller J.C.;
RT "Intra- and interbacterial genetic exchange of Lyme disease spirochete
  erp genes generates sequence identity amidst diversity.";
RL J. Mol. Evol. 57:309-324 (2003).
DR EMBL; AF022479; AAC35438.1; -.
DR EMBL; AY142091; AAN17865.1; -.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 9 AA; 1155 MW; 4E1A244330504373 CRC64;

Query Match 36.8%; Score 21; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WTVRN 5
DB 3 WIKN 7

RESULT 13
Q37854 PRELIMINARY; PRT; 8 AA.
AC Q37854;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Coliphage gene of unknown function, 5'end. (Fragment).
OS Bacteriophage R17.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
  Levivirus.
OX NCBI_TaxID=12026;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=73224987; PubMed=4352721;
RA Rensing U.F.E.;
RT "A sequence of seventy-three nucleotides from the coliphage R17
  genome.";
RL Biochem. J. 131:593-604 (1973).
DR EMBL; M24820; AAA72755.1; -.
FT NON_TER
SQ SEQUENCE 8 AA; 969 MW; ECB45412C1E72726 CRC64;

Query Match 33.3%; Score 19; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 3 VRNS 6
 Db ||||
 5 VRNS 8

RESULT 14
 Q8GL21
 ID_ Q8GL21 PRELIMINARY; PRT; 8 AA.
 AC Q8GL21; 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PF-50 protein (Fragment).
 GN Name=PF-50;
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OG Plasmid group cp32-8.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sh-2-82;
 RX MEDLINE=22990544; PubMed=14629041;
 RA Stevenson B., Miller J.C.;
 RT "Intra- and interbacterial genetic exchange of Lyme disease spirochete
 erp genes generates sequence identity amidst diversity.";
 RL J. Mol. Evol. 57:309-324(2003).
 DR EMBL; AY142094; AAN17903.1; -.
 KW Plasmid.
 FT NON TER 1 1
 SQ SEQUENCE 8 AA; 1042 MW; 1437244337204373 CRC64;

Query Match 33.3%; Score 19; DB 2; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WTVRN 5
 Db |::|
 2 WILKN 6

RESULT 15
 AKH_HELZE
 ID_AKH_HELZE STANDARD; PRT; 9 AA.
 AC P67787; P08901;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Adipokinetic hormone (Hez-AKH).
 OS Heliothis zea (Corn earworm) (Bollworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
 OC Noctuidae; Heliothinae; Helicoverpa.
 OX NCBI_TaxID=7113;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86186794; PubMed=3964263;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Holman G.M.,
 RA Wagner R.M., Ridgway R.L., Hayes D.K.;
 RT "Isolation and primary structure of a peptide from the corpora
 cardiaca of Heliothis zea with adipokinetic activity.";
 RL Biochem. Biophys. Res. Commun. 135:622-628(1986).
 CC -1- FUNCTION: This hormone, released from cells in the corpora
 cardiaca after the beginning of flight, causes release of
 diglycerides from the fat body and then stimulates the flight
 muscles to use these diglycerides as an energy source.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
 DR PIR; A24244; A24244.
 DR InterPro; IPR02047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Amidation; direct protein sequencing; Flight; Neuropeptide;
 KW Pyrrolidone carboxylic acid. Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1

FT MOD_RES 9 9 Glycine amide.
 SQ SEQUENCE 9 AA; 1026 MW; 403665A5A1A9D1A7 CRC64;
 Query Match 33.3%; Score 19; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVRNSW 7
 Db |::|
 3 TFTSSW 8

Search completed: May 19, 2005, 18:25:45
 Job time : 175 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 18:11:02 ; Search time 160 Seconds
(without alignments)
21.755 Million cell updates/sec

Title: US-09-867-159A-5

Perfect score: 57

Sequence: 1 WTVRNSWDT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 330156

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	57	100.0	9	5 AAO20571	Cysteine
2	57	100.0	9	5 ABB98536	Cysteine
3	41	71.9	8	5 ABJ04065	Cysteine
4	37	64.9	8	2 AAR77352	Cysteine
5	36	63.2	9	4 AAB76056	Trypanosoma
6	33	57.9	9	2 AAW60399	Tumour ho
7	33	57.9	9	2 AAW93726	Mouse B16
8	33	57.9	9	3 AAB21816	Murine me
9	33	57.9	9	4 AAE06394	Tumour ho
10	30	52.6	5	4 AAB85132	C. parvum
11	30	52.6	5	5 ABJ04066	Cysteine
12	30	52.6	5	8 ADQ95813	Cryptospor
13	29	50.9	7	8 ADH12805	Abalone c
14	29	50.9	8	4 AAB85131	P. vincke
15	29	50.9	8	8 ADQ95812	Cryptospor
16	29	50.9	9	8 ADK10416	Human pap
17	29	50.9	9	8 ADK10223	Human pap
18	28	49.1	9	7 ADM18218	Chlamydia
19	28	49.1	9	8 ADR23828	Human CNT
20	27	47.4	6	2 AAR57079	Fasciola
21	27	47.4	9	5 AAU71234	Human MHC
22	26	45.6	7	5 ABG60349	Selective
23	26	45.6	8	7 ADL17323	Human scr
24	26	45.6	9	4 AAB66538	Phage clo
25	26	45.6	9	5 ABG97265	Human leu

26	26	45.6	9	5 ABJ16457	Abj16457 Zinc tran
27	26	45.6	9	5 ABJ15476	Abj15476 Zinc tran
28	26	45.6	9	6 ABJ38076	Abj38076 Human cyt
29	26	45.6	9	8 ADN64445	ADN64445 HLA bindi
30	26	45.6	9	8 ADP30382	ADP30382 Human sec
31	26	45.6	9	8 ADR23827	ADR23827 Human CNT
32	25	43.9	7	2 AAW30429	AAW30429 HRE-I aff
33	25	43.9	8	3 AAY77698	Aay77698 TSG-6 bin
34	25	43.9	9	4 AAU24450	Aau24450 Human MHC
35	25	43.9	9	4 AAU24036	Aau24036 Human MHC
36	25	43.9	9	4 AAU23831	Aau23831 Human MHC
37	25	43.9	9	4 AAU24154	Aau24154 Human MHC
38	25	43.9	9	5 ABG34271	ABG34271 Human leu
39	25	43.9	9	7 ADK23765	ADK23765 Human 98P
40	25	43.9	9	8 ADK02690	ADK02690 Hepatitis
41	25	43.9	9	8 ADK07503	ADK07503 Hepatitis
42	24	42.1	7	2 AAY30217	Aay30217 Physarum
43	24	42.1	7	7 ADC54100	ADC54100 Commam am
44	24	42.1	7	7 ADL17066	ADL17066 Phage-dis
45	24	42.1	8	4 AAB78541	Aab78541 HIV-2 gp

ALIGNMENTS

RESULT 1

AAO20571
ID AAO20571 standard; peptide; 9 AA.

XX AC AAO20571;

XX DT 02-JAN-2003 (first entry)

XX DE Cysteine protease epitope peptide region, SEQ ID No 5.

XX KW Antiallergic; antiinflammatory; antiasthmatic; dermatological; allergen;
XX KW anti-histamine; histamine synthesis inhibitor; allergic hypersensitivity;
XX KW allergic asthma; allergic rhinitis; cysteine protease protein; enzyme;
XX KW atopic eczema; epitope.

XX OS Dermatophagoides pteronyssinus.

XX PN W0200278736-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-FR001098.

XX PR 30-MAR-2001; 2001FR-00004370.

XX PR 03-MAY-2001; 2001FR-00005929.

XX PR 29-MAY-2001; 2001US-00867159.

XX PA (ANTI-) ANTIALIS SARL.

XX PI Loria E, Terrasse G, Trehin Y;

XX DR WPI; 2002-750636/81.

XX PT Antiallergic compositions containing an anti-histamine, a histamine
XX PT synthesis inhibitor, and optionally an allergen or nucleic acid coding
XX PT for the allergen.

XX PS Claim 14; Page 11; 32pp; French.

XX CC The invention relates to antiallergic compositions containing an anti-
XX CC histamine, a histamine synthesis inhibitor, and optionally an allergen or
XX CC isolated nucleic acid molecule that has at least one polynucleotide
XX CC sequence coding for the allergen, together with a pharmaceutical carrier.
XX CC The pharmaceutical composition of the invention is useful as a non-
XX CC specific antiallergic treatment, and also useful in the treatment of
XX CC allergic hypersensitivity, allergic asthma, allergic rhinitis, and
XX CC allergic and atopic eczema. This sequence represents a peptide of a
XX CC cysteine protease epitope region relating to the antiallergic

CC compositions of the invention
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 57; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WTVRNSWDT 9
 |||||
 Db 1 WTVRNSWDT 9

RESULT 2
 ABB98536
 ID ABB98536 standard; peptide; 9 AA.

XX AC ABB98536;
 XX 13-DEC-2002 (first entry)
 XX Cysteine protease epitope #3.

XX Antiallergic; antiasthmatic; antiinflammatory; dermatological;
 KW immunotherapy; allergen; allergic hypersensitivity reaction;
 KW allergic asthma; allergic rhinitis; allergic atopic eczema;
 KW cysteine protease.

XX OS Dermatophagoides pteronyssinus.
 XX FR2822709-A1.

XX PN
 XX PD 04-OCT-2002.

XX PF 03-MAY-2001; 2001FR-00005929.

XX PR 30-MAR-2001; 2001FR-00004370.

XX PA (ANTI-) ANTIALIS SARL.

XX PI Loria E, Terrasse G, Trehin Y;

XX WPI; 2002-735037/80.

XX Antiallergic composition, useful for preventing and treating e.g. asthma,
 PT rhinitis or eczema, containing at least two of allergen, antihistamine
 PT and histamine synthesis inhibitor.

XX PS Claim 8; Page 6; 33pp; French.

XX The present invention relates to an antiallergic pharmaceutical
 CC composition (I) comprising a pharmaceutical carrier containing an active
 CC agent combination of at least two of: an allergen; an antihistamine; and
 CC a histamine synthesis inhibitor. (I) is used for treating or preventing
 CC allergic hypersensitivity reactions, especially allergic asthma, allergic
 CC rhinitis or allergic atopic eczema, in babies, children or adults. The
 CC present sequence is a peptide fragment (epitope) of cysteine protease
 CC from Dermatophagoides pteronyssinus, which was used as an allergen in the
 CC invention

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 57; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WTVRNSWDT 9
 |||||
 Db 1 WTVRNSWDT 9

RESULT 3
 ABJ04065

ID ABJ04065 standard; peptide; 8 AA.
 XX
 AC ABJ04065;

XX 27-SEP-2002 (first entry)

XX C parvum cryptopain peptide fragment SEQ ID NO: 112.

XX Cryptosporidium detection; GP900; P68; cryptopain; cryptosporidiosis.
 XX Cryptosporidium parvum.

XX OS WO200194631-A1.

XX PN 13-DEC-2001.

XX 14-MAY-2001; 2001WO-US015624.

XX PR 06-JUN-2000; 2000US-00588995.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Petersen C, Barnes DA, Nelson RG, Gut J;

XX WPI; 2002-566447/60.

XX Detecting Cryptosporidium in biological and environmental samples and
 PT diagnosis of cryptosporidiosis involves, contacting the sample with
 PT Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or RNA.
 XX Example 18; Page 154; 157pp; English.

XX The present invention relates to a method of detecting Cryptosporidium in
 CC biological and environmental samples, and of diagnosing
 CC cryptosporidiosis. This involves obtaining a sample and contacting it
 CC with Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or
 CC RNA, or its variant, mutant or fragment. The method is also useful for
 CC detecting and identifying individual Cryptosporidium isolates based on
 CC the genetic characteristics, and for diagnosis of prior or concurrent
 CC Cryptosporidium infection. The present sequence is a C. parvum peptide
 CC sequence used in the exemplification of the invention

XX SQ Sequence 8 AA;

Query Match 71.9%; Score 41; DB 5; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WTVRNSW 7
 |||||
 Db 2 WTVRNSW 8

RESULT 4

AAR77352

ID AAR77352 standard; peptide; 8 AA.

XX AAR77352;

XX 14-MAY-1996 (first entry)

XX Cysteine proteinase derived peptide #3.

XX Primer; amplify; polymerase chain reaction; PCR; Haemonchus contortus;
 KW cysteine proteinase; DM.2; DM.3; DM.4; human; DM.4a; DM.5; antigen;
 KW vaccine; helminth; parasite; DM.1; ruminant; gastro-intestinal tract.
 XX Haemonchus contortus.

XX PN WO9526402-A1.

XX 05-OCT-1995.

XX

```

PF 24-MAR-1995; 95WO-GB0000665.
XX
XX 25-MAR-1994; 94GB-00005925.
PR 25-MAR-1994; 94GB-00005990.
XX
XX (MLCW ) MALLINCKRODT VETERINARY INC.
XX
XX Knox DP, Smith SK, Smith WD, Redmond D, Murray J;
XX
XX WPI; 1995-351322/45.
DR N-PSDB; AAQ94242.
XX
XX Protective helminth parasite antigen - used in vaccine directed against
PT parasitic nematodes of mammalian gastro-intestinal tract e.g. Haemonchus
PT contortus.
XX
XX Example 16; Fig 15; 79pp; English.
XX
XX The sequences given in AAR77350-53 are peptides derived from the
CC canonical Haemonchus contortus cysteine proteinase molecule which were
CC used in the design of the primers given in AAQ94240-43. These primers
CC were used in the cloning of cDNA fragments from the cysteine proteinase
CC gene, such as DM.1, DM.2, DM.3, DM.4, DM.4a and DM.5 (see also AAQ94246-
CC 51). The amplified fragments may be expressed in a recombinant cell for
CC the production of antigens. These antigens may be used in the preparation
CC of a vaccine against helminth parasites in a human or non-human animal
XX
XX Sequence 8 AA;
SQ
Query Match 64.9%; Score 37; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WTVRNSW 7
DB 2 WIVKNSW 8
| : : : : |
| : : : : |

RESULT 5
AAB76056
ID AAB76056 standard; peptide; 9 AA.
XX
XX AAB76056;
AC
XX
XX 10-APR-2001 (first entry)
XX
XX Trypanosoma cruzi HLA-A2 binding peptide.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
XX cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
XX HLA binding peptide; immune response; glycoprotein; cytostatic; virucide;
XX hepatotropic; antiinflammatory; anti-HIV; vaccine;
XX human immunodeficiency virus; proteoacide; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;
XX cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
XX renal carcinoma; cervical carcinoma; lymphoma; malaria;
XX condyloma acuminatum.
XX
XX Trypanosoma cruzi.
XX
XX WO200100225-A1.
XX
XX 04-JAN-2001.
XX
XX 28-JUN-2000; 2000WO-US017842.
XX
XX 29-JUN-1999; 99US-0141422P.
XX
XX (EPIM-) EPIIMUNE INC.
XX
XX Sette A, Sidney J, Southwood S;
XX
XX WPI; 2001-112389/12.
XX

Composition comprising human leukocyte antigen binding peptide which
comprises isolated, prepared epitope useful for treating viral infections
such as acquired immunodeficiency syndrome, and cancer.
Claim 1; Page 46; 58pp; English.
The present invention describes a composition (I) which comprises at
least one human leukocyte antigen (HLA) binding peptide comprising an
isolated, prepared epitope comprising one of 547 8-11 residue amino acid
sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic,
CC virucide, hepatotropic, antiinflammatory, anti-HIV (human
CC immunodeficiency virus), and protozoacide activities, which can be used in
CC vaccine production and is an inducer of cytotoxic T-cell response. (I) is
CC useful for inducing a cytotoxic T cell response against a preselected
CC antigen in a patient expressing a specific major histocompatibility
CC complex (MHC) class I allele, by contacting cytotoxic T cells (CTLs) from
CC the patient with (I). (I) is useful as a vaccine to treat and/or prevent
CC viral infection and cancer such as prostate cancer, hepatitis B,
CC hepatitis C, human papilloma virus (HPV) infection, cytomegalovirus
CC (CMV), acquired immunodeficiency syndrome (AIDS), renal carcinoma,
CC cervical carcinoma, lymphoma, malaria, and condyloma acuminatum
XX
XX Sequence 9 AA;
SQ
Query Match 63.2%; Score 36; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WTVRNSW 7
DB 1 WIKNSW 7
| : : : : |
| : : : : |

RESULT 6
AAB60399
ID AAB60399 standard; peptide; 9 AA.
XX
XX AAB60399;
AC
XX
XX 24-AUG-1998 (first entry)
XX
XX Tumour homing peptide of the invention.
XX
XX Tumour homing peptide; in vivo panning; murine melanoma; tumour.
XX
XX Synthetic.
XX
XX WO9810795-A2.
XX
XX 19-MAR-1998.
XX
XX 10-SEP-1997; 97WO-US016086.
XX
XX 10-SEP-1996; 96US-00710067.
XX
XX (BURN-) BURNHAM INST.
XX
XX Ruoslahti E, Pasqualini R;
XX
XX WPI; 1998-207151/18.
XX
XX Tumour homing molecules and their conjugates - useful for, e.g. directing
XX linked moiety to tumour containing angiogenic vasculature.
XX
XX Example 5; Page 80; 105pp; English.
XX
XX AAB60390-432 represent peptides recovered from mouse melanomas. The
XX peptides are tumour homing peptides, and are identified by in vivo
XX panning. The in vivo panning comprises administering a library of diverse
XX peptides to a subject having a tumour, collecting a sample of the tumour,
XX identifying a peptide that homes to the tumour, collecting a sample of
XX normal tissue corresponding to the tumour, and determining that the

```

CC peptide that homes to the tumour is not present in the normal tissue. The
 CC tumour homing peptides can be linked to a moiety (e.g. doxorubicin), and
 CC used to direct the moiety to a tumour

XX
 SQ Sequence 9 AA;

Query Match 57.9%; Score 33; DB 2; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WTVRNSW 7
 ||| |||
 Db 1 WTCRASW 7

RESULT 7
 AAW93726
 ID AAW93726 standard; peptide; 9 AA.
 XX
 AC AAW93726;
 XX
 XX 28-JUN-1999 (first entry)
 DT
 XX
 DE Mouse B16B15b melanoma derived tumour homing peptide 11.
 XX
 KW Tumour homing peptide; tumour; diagnosis; endothelial cell; melanoma;
 KW angiogenic vasculature; anti-tumour; anti-inflammatory; anti-angiogenic;
 KW anti-arthritis; NGR receptor; inhibitor; angiogenesis; anticancer drug;
 KW prognosis; inflammation; regeneration; wounded tissue; targeting;
 KW macular degeneration; diabetic retinopathy; rheumatoid arthritis;
 KW occlusive thrombus; murine.
 XX
 OS Mus sp.
 XX
 XX WO9913329-A1.
 PN
 XX 18-MAR-1999.
 PD
 XX 08-SEP-1998; 98WO-US018895.
 PF
 XX 10-SEP-1997; 97US-00926914.
 PR
 XX 25-AUG-1998; 98US-00139802.
 PR
 XX (BURN-) BURNHAM INST.
 PA
 XX Ruoslahti E, Pasqualini R;
 PI
 XX WPI; 1999-215158/18.
 DR
 XX Identifying molecules that home to angiogenic vasculature used as targets
 for anticancer agents.
 PT
 XX Example VI; Page 115; 180pp; English.
 PS
 XX This invention describes novel peptides which home to angiogenic
 CC vasculature, specifically of a tumour and which have anti-tumour, anti-
 CC inflammatory, anti-angiogenic and anti-arthritis activity. Such molecules
 CC are identified by treating a purified NGR receptor with a test compound
 CC and identifying compounds that bind specifically to the NGR receptor. The
 CC peptides of the invention are inhibitors of angiogenesis and can be used
 CC to produce conjugates for delivering agents to angiogenic vasculature,
 CC particularly anticancer drugs or an imaging agent, for diagnosis or
 CC prognosis. These conjugates may be directed to non-tumour angiogenic
 CC vasculature, e.g. that present in inflammatory, regenerating or wounded
 CC tissue, e.g. for treatment of macular degeneration, diabetic retinopathy
 CC or rheumatoid arthritis. The peptides provide specific targeting to
 CC tumours, especially their supporting vasculature, since the NGR receptor
 CC is exposed to the circulation only in angiogenic vasculature. Precise
 CC targeting should reduce the systemic toxicity of anticancer drugs in the
 CC conjugates. Complete killing of all target cells may not be essential
 CC since partial denudation of endothelium may result in an occlusive
 CC thrombus, and endothelial cells are unlikely to become resistant to
 CC anticancer agents nor to lose the targeting receptor. AAW93622-W93809 and

CC AAW93843-44 are examples of tumour homing peptides used in the invention

XX
 SQ Sequence 9 AA;

Query Match 57.9%; Score 33; DB 2; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WTVRNSW 7
 ||| |||
 Db 1 WTCRASW 7

RESULT 8
 AAB21816
 ID AAB21816 standard; peptide; 9 AA.
 XX
 AC AAB21816;
 XX
 XX 22-MAR-2001 (first entry)
 DT
 XX Murine melanoma homing peptide #11.
 DE
 XX Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial;
 KW breast; prostate; melanoma; cancer; Kaposi's sarcoma; murine.
 XX
 OS Mus sp.
 XX
 PN WO200042973-A2.
 XX
 PD 27-JUL-2000.
 XX
 XX 21-JAN-2000; 2000WO-US001602.
 PF
 XX 22-JAN-1999; 99US-00235902.
 PR
 XX (BURN-) BURNHAM INST.
 PA
 XX Ellerby HM, Bredeesen DE, Pasqualini R, Ruoslahti EI;
 PI
 XX WPI; 2000-499174/44.
 DR
 XX Homing pro-apoptotic conjugate comprising a tumor homing molecule that
 PT selectively homes to a mammalian cell type or tissue linked to an
 PT antimicrobial peptide, useful for the treatment of prostate cancer.
 XX
 PS Example 8; Page 96; 118pp; English.
 XX
 CC The present invention relates to homing pro-apoptotic conjugates,
 CC comprising of a tumour homing molecule that selectively homes to a
 CC mammalian cell type or tissue, linked to an antimicrobial peptide. The
 CC homing pro-apoptotic conjugates are selectively internalised by the
 CC mammalian cell type or tissue and exhibits high toxicity, especially to
 CC angiogenic vasculature. The antimicrobial peptide has low mammalian cell
 CC toxicity when not linked to the tumor homing molecule. The conjugates are
 CC useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and
 CC prostate cancer or melanoma. The present sequence is a homing peptide
 CC isolated in the present invention, which can be conjugated to an
 CC antimicrobial peptide to make the homing pro-apoptotic conjugates of the
 CC present invention

XX
 SQ Sequence 9 AA;

Query Match 57.9%; Score 33; DB 3; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WTVRNSW 7
 ||| |||
 Db 1 WTCRASW 7

RESULT 9


```

AAE06394
ID AAE06394 standard; peptide; 9 AA.
XX
AC AAE06394;
XX
DT 25-SEP-2001 (first entry)
XX
DE Tumour homing peptide #11 from mouse B16B15b melanoma.
XX
KW Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide;
KW antimicrobial peptide; prostate cancer; tumour homing molecule; mouse;
KW cytostatic.
XX
OS Mus sp.
XX
PN WO200153342-A1.
XX
PD 26-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US001362.
XX
PR 21-JAN-2000; 2000US-00489582.
XX
PA (BURN-) BURNHAM INST.
XX
PI Ruoslahti EI, Pasqualini R, Arap W, Bredesen DE, Ellerby HM;
XX
DR WPI; 2001-451901/48.
XX
PT Novel chimeric prostate-homing pro-apoptotic peptide, used to treat
PT prostate cancer, comprises a prostate-homing peptide linked to an
PT antimicrobial peptide.
XX
PS Example 8; Page 95; 176pp; English.
XX
CC The patent discloses novel chimeric prostate-homing pro-apoptotic peptide
CC which comprises a prostate-homing peptide linked to an antimicrobial
CC peptide, where the chimeric peptide is selectively internalised by and
CC exhibits high toxicity to prostate tissue and where the antimicrobial
CC peptide has low mammalian cell toxicity when not linked to prostate-
CC homing peptide. The chimeric peptide is used to direct an antimicrobial
CC peptide in vivo to a prostate cancer, to induce selective toxicity in
CC vivo in a prostate cancer, and to treat a patient with prostate cancer.
CC The present sequence is a tumour homing peptide from mouse B16B15b
CC melanoma. This sequence is useful in the homing of pro-apoptotic
CC conjugates of the invention
XX
SQ Sequence 9 AA;
Query Match 57.9%; Score 33; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 WTVNSW 7
DB 1 WTCRASW 7
RESULT 10
AAB85132
ID AAB85132 standard; peptide; 5 AA.
XX
AC AAB85132;
XX
DT 22-AUG-2001 (first entry)
XX
DE C. parvum cryptopain protein fragment.
XX
KW Cryptosporidium; infection; cryptopain; antiparasitic; vaccine;
KW immunization.
XX
OS Cryptosporidium parvum.
XX
PN
PD
PF
PR
PS
PT
QY
DB

```

```

PN US6254869-B1.
XX
PD 03-JUL-2001.
XX
PF 27-MAR-1997; 97US-00827171.
XX
PR 27-MAR-1996; 96US-0014233P.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Petersen C, Huang J;
XX
DR WPI; 2001-388923/41.
XX
PT New vaccines and cryptopain protein for diagnosis and treatment of
PT Cryptosporidium species infection.
XX
PS Example 2; Col 19; 32pp; English.
XX
CC The invention relates to vaccines and cryptopain protein for diagnosis
CC and treatment of Cryptosporidium species infection. Cryptopain protein
CC can be expressed by standard recombinant methodology. The vaccines
CC comprising the cryptopain protein or its fragments are useful for active
CC immunization of animals and humans against Cryptosporidium infection, or
CC for production of passive immune products in admixture with an adjuvant.
CC Cryptopain can be used for prophylactic, therapeutic, diagnostic and
CC detection purposes. The present sequence represents a peptide fragment of
CC the C. parvum cryptopain protein
XX
SQ Sequence 5 AA;
Query Match 52.6%; Score 30; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 VRNSW 7
DB 1 VRNSW 5
RESULT 11
ABJ04066
ID ABJ04066 standard; peptide; 5 AA.
XX
AC ABJ04066;
XX
DT 27-SEP-2002 (first entry)
XX
DE C parvum cryptopain peptide fragment SEQ ID NO: 113.
XX
KW Cryptosporidium detection; GP900; P68; cryptopain; cryptosporidiosis.
XX
OS Cryptosporidium parvum.
XX
PN WO200194631-A1.
XX
PD 13-DEC-2001.
XX
PF 14-MAY-2001; 2001WO-US015624.
XX
PR 06-JUN-2000; 2000US-00588995.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Petersen C, Barnes DA, Nelson RG, Gut J;
XX
DR WPI; 2002-566447/60.
XX
PT Detecting Cryptosporidium in biological and environmental samples and
PT diagnosis of cryptosporidiosis involves, contacting the sample with
PT Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or RNA.
XX
PS Disclosure; Page 154; 157pp; English.

```



```

RESULT 14
AAB85131
ID AAB85131 standard; peptide; 8 AA.
XX
XX AAB85131;
AC
XX
XX 22-AUG-2001 (first entry)
DT
XX
XX P. vinckei cysteine proteinase conserved motif.
DE
XX
XX Cryptosporidium; infection; cryptopain; antiparasitic; vaccine;
KW immunization; cysteine proteinase.
KW
XX
XX Plasmodium vinckei.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 4
FT /label= Val or Ile
FT
FT Misc-difference 5
FT /label= Lys or Arg
FT
XX
XX US6254869-B1.
PN
XX
XX 03-JUL-2001.
PD
XX
XX 27-MAR-1997; 97US-00827171.
PF
XX
XX 27-MAR-1996; 96US-0014233P.
PR
XX
XX (REGC ) UNIV CALIFORNIA.
PA
XX
XX Petersen C, Huang J;
PI
XX
XX WPI; 2001-388923/41.
DR
XX
XX New vaccines and cryptopain protein for diagnosis and treatment of
PT Cryptosporidium species infection.
PT
XX
XX Example 2; Col 19; 32pp; English.
PS
XX
XX The invention relates to vaccines and cryptopain protein for diagnosis
CC and treatment of Cryptosporidium species infection. Cryptopain protein
CC can be expressed by standard recombinant methodology. The vaccines
CC comprising the cryptopain protein or its fragments are useful for active
CC immunization of animals and humans against Cryptosporidium infection, or
CC for production of passive immune products in admixture with an adjuvant.
CC Cryptopain can be used for prophylactic, therapeutic, diagnostic and
CC detection purposes. The present sequence represents a conserved motif
CC from P. vinckei cysteine proteinase, used for designing degenerate
CC primers for amplifying DNA fragments of C. parvum cryptopain gene
XX
XX
XX Sequence 8 AA;
Query Match 50.9%; Score 29; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WTVRNSW 7
Db | |||
2 WIXXNSW 8

Search completed: May 19, 2005, 18:22:51
Job time : 168 secs

RESULT 15
ADQ95812
ID ADQ95812 standard; peptide; 8 AA.
XX
XX ADQ95812;
AC
XX
XX 23-SEP-2004 (first entry)
DT
XX
XX Cryptosporidium parvum cryptopain fragment #2.
DE
XX
XX Cryptosporidium infection; antigen; cryptopain;
KW

```

```

KW
XX
XX cathepsin L-like cysteine proteinase; passive immunity; vaccine; enzyme.
OS
XX
XX Cryptosporidium parvum.
FH
XX
XX Key Location/Qualifiers
FT Misc-difference 4 /label= Val, Ile
FT
FT Misc-difference 5 /label= Lys, Arg
FT
XX
XX US6759044-B1.
PN
XX
XX 06-JUL-2004.
PD
XX
XX 20-JUN-2000; 2000US-00598062.
PF
XX
XX 27-MAR-1996; 96US-0014233P.
PR
XX
XX 27-MAR-1997; 97US-00827171.
XX
XX (REGC ) UNIV CALIFORNIA.
PA
XX
XX Petersen C, Huang J;
PI
XX
XX WPI; 2004-515391/49.
DR
XX
XX New cryptopain antibodies, useful for treating or inhibiting
PT Cryptosporidium infection, or as vaccine for to provide passive immunity
PT to Cryptosporium infection.
PT
XX
XX Example 2; SEQ ID NO 14; 33pp; English.
PS
XX
XX The invention relates to an antibody produced against and binding to
CC Cryptosporidium antigen, cryptopain. The invention also provides
CC polynucleotides encoding cryptopain which is a cathepsin L-like cysteine
CC proteinase. The antibody is useful for detecting and treating
CC Cryptosporidium infection, for providing passive immunity or for
CC inhibiting existing Cryptosporidium infection. The present sequence is
CC Cryptosporidium parvum cryptopain fragment.
XX
XX
XX Sequence 8 AA;
Query Match 50.9%; Score 29; DB 8; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WTVRNSW 7
Db | |||
2 WIXXNSW 8

Search completed: May 19, 2005, 18:22:51
Job time : 168 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 18:25:53 ; Search time 132 Seconds
(without alignments)
22.807 Million cell updates/sec

Title: US-09-867-159A-5

Perfect score: 57

Sequence: 1 WTVRNSWDT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 141056

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PTCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	9	10	US-09-867-159A-5
2	33	57.9	9	9	US-09-765-086-116
3	33	57.9	9	14	US-10-264-374-116
4	33	57.9	9	14	US-10-375-992-116
5	33	57.9	9	15	US-10-264-374-116
6	33	57.9	9	16	US-10-375-992-116
7	28	49.1	9	17	US-10-888-348-25
8	27	47.4	9	9	US-09-834-765-155
9	26	45.6	7	16	US-10-363-204-24
10	26	45.6	8	14	US-10-190-082-286
11	26	45.6	9	15	US-10-024-652-130
12	26	45.6	9	15	US-10-024-652-981
13	26	45.6	9	17	US-10-482-284A-134

14	26	45.6	9	17	US-10-888-348-24	Sequence 24, Appl
15	25	43.9	9	10	US-09-793-451-30	Sequence 30, Appl
16	25	43.9	9	10	US-09-793-451-235	Sequence 235, App
17	25	43.9	9	10	US-09-793-451-353	Sequence 353, App
18	25	43.9	9	10	US-09-793-451-649	Sequence 649, App
19	25	43.9	9	10	US-09-942-052-119	Sequence 119, App
20	25	43.9	9	14	US-10-283-722-30	Sequence 30, Appl
21	25	43.9	9	14	US-10-283-722-235	Sequence 235, App
22	25	43.9	9	14	US-10-283-722-353	Sequence 353, App
23	25	43.9	9	14	US-10-283-722-649	Sequence 649, App
24	25	43.9	9	15	US-10-283-903-30	Sequence 30, Appl
25	25	43.9	9	15	US-10-283-903-235	Sequence 235, App
26	25	43.9	9	15	US-10-283-903-353	Sequence 353, App
27	25	43.9	9	15	US-10-283-903-649	Sequence 649, App
28	25	43.9	9	17	US-10-808-187-677	Sequence 677, App
29	24	42.1	7	14	US-10-190-082-16	Sequence 16, Appl
30	24	42.1	8	14	US-10-351-641-1643	Sequence 1643, Ap
31	24	42.1	9	15	US-10-334-726-184	Sequence 184, App
32	24	42.1	9	15	US-10-334-726-295	Sequence 295, App
33	24	42.1	9	15	US-10-609-217-664	Sequence 664, App
34	24	42.1	9	15	US-10-632-388-664	Sequence 664, App
35	24	42.1	9	15	US-10-651-723-664	Sequence 664, App
36	24	42.1	9	15	US-10-645-761-664	Sequence 664, App
37	24	42.1	9	15	US-10-666-696-664	Sequence 664, App
38	24	42.1	9	15	US-10-653-048-664	Sequence 664, App
39	23	40.4	5	16	US-10-705-195-17	Sequence 17, Appl
40	23	40.4	5	16	US-10-714-564A-471	Sequence 471, App
41	23	40.4	6	14	US-10-072-602B-626	Sequence 626, App
42	23	40.4	6	14	US-10-072-602B-628	Sequence 628, App
43	23	40.4	7	14	US-10-072-602B-627	Sequence 627, App
44	23	40.4	7	14	US-10-190-082-129	Sequence 129, App
45	23	40.4	7	14	US-10-190-082-133	Sequence 133, App

ALIGNMENTS

RESULT 1

US-09-867-159A-5
; Sequence 5, Application US/09867159A
; Publication No. US20030104013A1
; GENERAL INFORMATION:
; APPLICANT: ANTIALIS TERRASSE, GAETAN LORIA, EMILE TREHIN, YVES
; TITLE OF INVENTION: Anti-allergic pharmaceutical composition containing at least one
; TITLE OF INVENTION: and at least one anti-histamine compound
; FILE REFERENCE: B112812US-antialis
; CURRENT APPLICATION NUMBER: US/09/867,159A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: FR01/04370
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: FR01/05929
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Dermatophagoides pteromyssinus
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: Comprises epitope from cystine protease.
US-09-867-159A-5

Query Match 100.0%; Score 57; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTVRNSWDT 9

Db 1 WTVRNSWDT 9

RESULT 2

US-09-765-086-116
; Sequence 116, Application US/09765086
; Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Wadib, Arap
; APPLICANT: Bredeesen, Dale E.
; APPLICANT: Ellerby, H. Michael
; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
; FILE REFERENCE: P-LJ 3844
; CURRENT FILING DATE: 2001-01-17
; CURRENT APPLICATION NUMBER: US/09/765,086
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/489,582
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-765-086-116

Query Match 57.9%; Score 33; DB 9; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WTVRNSW 7
|||
Db 1 WTCRASW 7

RESULT 3

US-10-264-374-116
; Sequence 116, Application US/10264374
; Publication No. US20030113320A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/10/264,374
; CURRENT FILING DATE: 2002-10-03
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/139,802
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-264-374-116

Query Match 57.9%; Score 33; DB 14; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WTVRNSW 7
|||
Db 1 WTCRASW 7

RESULT 4

US-10-375-992-116
; Sequence 116, Application US/10375992
; Publication No. US20030152578A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
; FILE REFERENCE: Derived Therefrom, and Methods of Using Same
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/375,992
; FILING DATE: 27-Feb-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,914
; FILING DATE: 10-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2725
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-375-992-116

Query Match 57.9%; Score 33; DB 14; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WTVRNSW 7
|||
Db 1 WTCRASW 7

RESULT 5

US-10-264-374-116
; Sequence 116, Application US/10264374
; Publication No. US20040096441A9
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/10/264,374
; CURRENT FILING DATE: 2002-10-03
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/139,802
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10

;; PRIOR APPLICATION NUMBER: 08/710,067
;; PRIOR FILING DATE: 1996-09-10
;; NUMBER OF SEQ ID NOS: 226
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 116
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: Peptide
US-10-264-374-116

Query Match 57.9%; Score 33; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WTVRNSW 7
|||
Db 1 WTCRASW 7

RESULT 6
US-10-375-992-116
;; Sequence 116, Application US/10375992
;; Publication No. US20040131623A9
;; GENERAL INFORMATION:
;; APPLICANT: Ruoslahti, Erkki
;; Pasaqualini, Renata
;; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
;; DERIVED THEREFROM, AND METHODS OF USING SAME
;; NUMBER OF SEQUENCES: 199
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Campbell & Flores
;; STREET: 4370 La Jolla Village Drive, Suite 700
;; CITY: San Diego
;; STATE: California
;; COUNTRY: United States
;; ZIP: 92122
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/375,992
;; FILING DATE: 27-Feb-2003
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/926,914
;; FILING DATE: 10-SEP-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-LJ 2725
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 116:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; TOPOLOGY: both
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-375-992-116

Query Match 57.9%; Score 33; DB 16; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WTVRNSW 7
|||
Db 1 WTCRASW 7

RESULT 7
US-10-888-348-25
;; Sequence 25, Application US/10888348
;; Publication No. US20050064555A1
;; GENERAL INFORMATION:
;; APPLICANT: Marshall, Shannon
;; APPLICANT: Barbosa, Maria
;; TITLE OF INVENTION: CILIARY NEUTROTROPHIC FACTOR VARIANTS
;; FILE REFERENCE: 34431/US
;; CURRENT APPLICATION NUMBER: US/10/888,348
;; CURRENT FILING DATE: 2004-07-09
;; PRIOR APPLICATION NUMBER: US 60/485,941
;; PRIOR FILING DATE: 2003-07-09
;; PRIOR APPLICATION NUMBER: US 60/528,229
;; PRIOR FILING DATE: 2003-12-08
;; NUMBER OF SEQ ID NOS: 165
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 25
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-888-348-25

Query Match 49.1%; Score 28; DB 17; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WTVRNSWD 8
|||
Db 1 WTVRSIHD 8

RESULT 8
US-09-834-765-155
;; Sequence 155, Application US/09834765
;; Patent No. US20020055478A1
;; GENERAL INFORMATION:
;; APPLICANT: Mary Faris
;; APPLICANT: Pia M. Challita-Eid
;; APPLICANT: Arthur B. Raitano
;; APPLICANT: Steve Chappell Mitchell
;; APPLICANT: Daniel E.H. Afar
;; APPLICANT: Ava Jakobovits
;; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
;; FILE REFERENCE: AND DETECTION OF CANCER
;; FILE REFERENCE: 129.6US01
;; CURRENT APPLICATION NUMBER: US/09/834,765
;; CURRENT FILING DATE: 2001-09-21
;; PRIOR APPLICATION NUMBER: 60/197,647
;; PRIOR FILING DATE: 2000-04-12
;; NUMBER OF SEQ ID NOS: 770
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 155
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-834-765-155

Query Match 47.4%; Score 27; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TVRNSWD 9
|||
Db 2 TVLQLWD 9

RESULT 9
US-10-363-204-24
;; Sequence 24, Application US/10363204

; Publication No. US20040170955A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: US/10/363,204
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(7)
; OTHER INFORMATION: synthetic construct
US-10-363-204-24

Query Match 45.6%; Score 26; DB 16; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WTVRN 5
|||:
Db 2 WTVRD 6

RESULT 10
US-10-190-082-286
; Sequence 286, Application US/10190082
; Publication No. US20030148264A1
; GENERAL INFORMATION:
; APPLICANT: Laeky, Lawrence A.
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Held, Heike A.
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
; FILE REFERENCE: P1905R1
; CURRENT APPLICATION NUMBER: US/10/190,082
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 286
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-190-082-286

Query Match 45.6%; Score 26; DB 14; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVRNSW 7
|||:
Db 2 TVRETW 7

RESULT 11
US-10-024-652-130
; Sequence 130, Application US/10024652
; Publication No. US20030219738A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Paris, Mary
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Mitchell, Steve Chappell
; APPLICANT: Levin, Elana
; APPLICANT: Morrison, Karen Jane Meyrick

; APPLICANT: Raitano, Arthur B.
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
; TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
; TITLE OF INVENTION: Detection of Cancer
; FILE REFERENCE: 51158-20025.00
; CURRENT APPLICATION NUMBER: US/10/024,652
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/256,210
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 2598
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapien
US-10-024-652-130

Query Match 45.6%; Score 26; DB 15; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TVRNSWDT 9
|||:
Db 2 TFRILIWD 9

RESULT 12
US-10-024-652-981
; Sequence 981, Application US/10024652
; Publication No. US20030219738A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Paris, Mary
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Mitchell, Steve Chappell
; APPLICANT: Levin, Elana
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
; TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
; TITLE OF INVENTION: Detection of Cancer
; FILE REFERENCE: 51158-20025.00
; CURRENT APPLICATION NUMBER: US/10/024,652
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/256,210
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 2598
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 981
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapien
US-10-024-652-981

Query Match 45.6%; Score 26; DB 15; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TVRNSWDT 9
|||:
Db 2 TFRILIWD 9

RESULT 13
US-10-482-284A-134
; Sequence 134, Application US/10482284A
; Publication No. US20050019344A1
; GENERAL INFORMATION:
; APPLICANT: KHANNA, Rajiv

; APPLICANT: ELKINGTON, Rebecca A.
; APPLICANT: WALKER, Susan J.
; TITLE OF INVENTION: Novel human cytomegalovirus (HCMV) cytotoxic T cell epitopes,
; TITLE OF INVENTION: polypeptides, compositions comprising same and diagnostic and th
; TITLE OF INVENTION: uses therefore
; FILE REFERENCE: 47-203
; CURRENT APPLICATION NUMBER: US/10/482,284A
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: AU PR5931
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 318
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 134
; LENGTH: 9
; TYPE: PRT
; ORGANISM: human cytomegalovirus pp150 CTL epitope peptide
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human cytomegalovirus pp65 C
; OTHER INFORMATION: epitope peptide
US-10-482-284A-134

Query Match 45.6%; Score 26; DB 17; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VRNSWD 8
|||
Db 2 VRRSWE 7

RESULT 14
US-10-888-348-24
; Sequence 24, Application US/10888348
; Publication No. US20050064555A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Shannon
; APPLICANT: Barbosa, Maria
; TITLE OF INVENTION: CILIARY NEUROTROPHIC FACTOR VARIANTS
; FILE REFERENCE: 34431/US
; CURRENT APPLICATION NUMBER: US/10/888,348
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/485,941
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/528,229
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-888-348-24

Query Match 45.6%; Score 26; DB 17; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTVRN 5
|||
Db 4 WTVRS 8

RESULT 15
US-09-793-451-30
; Sequence 30, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid

; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-30

Query Match 43.9%; Score 25; DB 10; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WTVRNSW 7
|||
Db 1 WTYSGOW 7

Search completed: May 19, 2005, 18:38:34
Job time : 133 secs

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OM protein - protein search, using sw model

Run on: May 19, 2005, 18:17:01 ; Search time 41 Seconds
(without alignments)
16.386 Million cell updates/sec

Title: US-09-867-159A-5

Perfect score: 57

Sequence: 1 WTVRNSWD 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 99282

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	71.9	8	4	US-09-588-995A-112
2	33	57.9	9	3	US-09-139-802-116
3	33	57.9	9	4	US-09-659-786-116
4	33	57.9	9	4	US-08-926-914-116
5	30	52.6	5	3	US-08-827-171B-15
6	30	52.6	5	4	US-09-588-995A-113
7	30	52.6	5	4	US-09-598-062-15
8	29	50.9	8	3	US-08-827-171B-14
9	29	50.9	8	4	US-09-598-062-14
10	26.5	46.5	9	2	US-08-706-741B-79
11	26.5	46.5	9	2	US-08-924-695A-79
12	24.5	43.0	9	2	US-08-733-050A-42
13	24.5	43.0	9	2	US-08-706-741B-77
14	24.5	43.0	9	2	US-08-924-695A-77
15	24	42.1	8	3	US-09-082-279B-1488
16	24	42.1	8	3	US-09-315-304B-1642
17	24	42.1	8	4	US-09-834-784-1488
18	24	42.1	8	4	US-09-350-641C-1643
19	24	42.1	9	1	US-08-190-788A-34
20	24	42.1	9	1	US-08-383-474B-39
21	24	42.1	9	1	US-08-465-391A-34
22	24	42.1	9	2	US-08-464-538B-34
23	24	42.1	9	2	US-08-463-076E-78
24	24	42.1	9	4	US-09-428-082B-664
25	23	40.4	5	4	US-09-807-063-17
26	23	40.4	8	3	US-09-082-279B-1483
27	23	40.4	8	3	US-09-082-279B-1484

28	23	40.4	8	3	US-09-082-279B-1486	Sequence 1486, Ap
29	23	40.4	8	3	US-09-082-279B-1489	Sequence 1489, Ap
30	23	40.4	8	3	US-09-082-279B-1499	Sequence 1499, Ap
31	23	40.4	8	3	US-09-315-304B-1562	Sequence 1562, Ap
32	23	40.4	8	3	US-09-315-304B-1637	Sequence 1637, Ap
33	23	40.4	8	3	US-09-315-304B-1638	Sequence 1638, Ap
34	23	40.4	8	3	US-09-315-304B-1639	Sequence 1639, Ap
35	23	40.4	8	3	US-09-315-304B-1640	Sequence 1640, Ap
36	23	40.4	8	3	US-09-315-304B-1653	Sequence 1653, Ap
37	23	40.4	8	4	US-09-360-545-46	Sequence 46, Appl
38	23	40.4	8	4	US-09-350-325-22	Sequence 22, Appl
39	23	40.4	8	4	US-09-834-784-1483	Sequence 1483, Ap
40	23	40.4	8	4	US-09-834-784-1484	Sequence 1484, Ap
41	23	40.4	8	4	US-09-834-784-1486	Sequence 1486, Ap
42	23	40.4	8	4	US-09-834-784-1489	Sequence 1489, Ap
43	23	40.4	8	4	US-09-834-784-1499	Sequence 1499, Ap
44	23	40.4	8	4	US-09-515-965A-1594	Sequence 1594, Ap
45	23	40.4	8	4	US-09-350-641C-1562	Sequence 1562, Ap

ALIGNMENTS

RESULT 1

US-09-588-995A-112
; Sequence 112, Application US/09588995A
; Patent No. 6514697
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: BARNES, DEBRA A.
; APPLICANT: NELSON, RICHARD C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: INFECTIONS
; FILE REFERENCE: 480.19-5
; CURRENT APPLICATION NUMBER: US/09/588,995A
; CURRENT FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 08/827,171
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/928,361
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 08/700,651
; PRIOR FILING DATE: 1996-08-14
; PRIOR APPLICATION NUMBER: 08/415,751
; PRIOR FILING DATE: 1995-04-03
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (3)_
; OTHER INFORMATION: L or I
US-09-588-995A-112

Query Match 71.9%; Score 41; DB 4; Length 8;
Best Local Similarity 85.7%; Pred No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTVRNSW 7
| | | | |
Db 2 WTVRNSW 8

RESULT 2

US-09-139-802-116
; Sequence 116, Application US/09139802
; Patent No. 6180084
; GENERAL INFORMATION:
; APPLICANT: Ruoslanti, Erkki

```
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/139,802
; EARLIER FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 08/926,914
; EARLIER FILING DATE: 1997-09-10
; EARLIER APPLICATION NUMBER: 08/710,067
; EARLIER FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-139-802-116

Query Match      57.9%; Score 33; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 WTVRNSW 7
      ||| |||
Db      1 WTCRASW 7

RESULT 3
US-09-659-786-116
; Sequence 116, Application US/09659786
; Patent No. 6491894
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/659,786
; EARLIER FILING DATE: 2000-09-11
; EARLIER APPLICATION NUMBER: 08/926,914
; EARLIER FILING DATE: 1997-09-10
; EARLIER APPLICATION NUMBER: 08/710,067
; EARLIER FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-659-786-116

Query Match      57.9%; Score 33; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 WTVRNSW 7
      ||| |||
Db      1 WTCRASW 7

RESULT 4
US-08-926-914-116
; Sequence 116, Application US/08926914
; Patent No. 6576239
; GENERAL INFORMATION:
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
; TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,914
; FILING DATE: 10-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2725
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
US-08-926-914-116

Query Match      57.9%; Score 33; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 WTVRNSW 7
      ||| |||
Db      1 WTCRASW 7

RESULT 5
US-08-827-171B-15
; Sequence 15, Application US/08827171B
; Patent No. 6254869
; GENERAL INFORMATION:
; APPLICANT: CAROLYN PETERSEN
; APPLICANT: JIN-XING HUANG
; TITLE OF INVENTION: CRYPTOPAIN VACCINES, ANTIBODIES, PROTEINS,
; TITLE OF INVENTION: PEPTIDES, DNA AND RNAs FOR PROPHYLAXIS,
; TITLE OF INVENTION: TREATMENT, DIAGNOSIS AND
; TITLE OF INVENTION: DETECTION OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIK A
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: California
; COUNTRY: United States of America
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
; COMPUTER: PC
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: Wordperfect 6.0a WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,171B
; FILING DATE:
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```
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
; TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,914
; FILING DATE: 10-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2725
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
US-08-926-914-116

Query Match      57.9%; Score 33; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 WTVRNSW 7
      ||| |||
Db      1 WTCRASW 7

RESULT 5
US-08-827-171B-15
; Sequence 15, Application US/08827171B
; Patent No. 6254869
; GENERAL INFORMATION:
; APPLICANT: CAROLYN PETERSEN
; APPLICANT: JIN-XING HUANG
; TITLE OF INVENTION: CRYPTOPAIN VACCINES, ANTIBODIES, PROTEINS,
; TITLE OF INVENTION: PEPTIDES, DNA AND RNAs FOR PROPHYLAXIS,
; TITLE OF INVENTION: TREATMENT, DIAGNOSIS AND
; TITLE OF INVENTION: DETECTION OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIK A
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: California
; COUNTRY: United States of America
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
; COMPUTER: PC
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: Wordperfect 6.0a WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,171B
; FILING DATE:
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; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/014,233
; FILING DATE: March 27, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hana Verny
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: (HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-1677
; TELEFAX: (415) 324-1678
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-827-171B-15

Query Match 52.6%; Score 30; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VRNSW 7
Db 1 VRNSW 5

RESULT 6
US-09-588-995A-113
; Sequence 113, Application US/09588995A
; Patent No. 6514697
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: BARNES, DEBRA A.
; APPLICANT: NELSON, RICHARD C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
; TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: INFECTIONS
; FILE REFERENCE: 480.19-5
; CURRENT APPLICATION NUMBER: US/09/588,995A
; CURRENT FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 08/827,171
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/928,361
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 08/700,651
; PRIOR FILING DATE: 1996-08-14
; PRIOR APPLICATION NUMBER: 08/415,751
; PRIOR FILING DATE: 1995-04-03
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
; US-09-588-995A-113

Query Match 52.6%; Score 30; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VRNSW 7
Db 1 VRNSW 5

RESULT 7
US-09-598-062-15
; Sequence 15, Application US/09598062
; Patent No. 6759044
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```
; GENERAL INFORMATION:
; APPLICANT: CAROLYN PETERSEN
; APPLICANT: JIN-XING HUANG
; TITLE OF INVENTION: CRYPTOPAIN VACCINES, ANTIBODIES, PROTEINS,
; PEPTIDES, DNA AND RNAs FOR PROPHYLAXIS,
; TREATMENT, DIAGNOSIS AND
; DETECTION OF
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIK A
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: California
; COUNTRY: United States of America
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
; COMPUTER: PC
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: Wordperfect 6.0a WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/598,062
; FILING DATE: 20-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,171
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 60/014,233
; FILING DATE: March 27, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hana Verny
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: (HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-1677
; TELEFAX: (415) 324-1678
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
; US-09-598-062-15

Query Match 52.6%; Score 30; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VRNSW 7
Db 1 VRNSW 5

RESULT 8
US-08-827-171B-14
; Sequence 14, Application US/08827171B
; Patent No. 6254869
; GENERAL INFORMATION:
; APPLICANT: CAROLYN PETERSEN
; APPLICANT: JIN-XING HUANG
; TITLE OF INVENTION: CRYPTOPAIN VACCINES, ANTIBODIES, PROTEINS,
; PEPTIDES, DNA AND RNAs FOR PROPHYLAXIS,
; TREATMENT, DIAGNOSIS AND
; DETECTION OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIK A
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: California
```

; COUNTRY: United States of America
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
; COMPUTER: PC
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: Wordperfect 6.0a WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,171B
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/014,233
; FILING DATE: March 27, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hana VERNY
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: (HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-1677
; TELEFAX: (415) 324-1678
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptides
; FEATURE:
; NAME/KEY: Xaa at 4 is Val/Ile
; NAME/KEY: Xaa at 5 is Lys/Arg
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; US-08-827-171B-14

Query Match 50.9%; Score 29; DB 3; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WTVRNSW 7
|
Db 2 WIXXNSW 8

RESULT 9

US-09-598-062-14
; GENERAL INFORMATION:
; APPLICANT: CAROLYN PETERSEN
; JIN-XING HUANG
; TITLE OF INVENTION: CRYPTOPAIN VACCINES, ANTIBODIES, PROTEINS,
; PEPTIDES, DNA AND RNAs FOR PROPHYLAXIS,
; TREATMENT, DIAGNOSIS AND
; DETECTION OF
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIK A
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: California
; COUNTRY: United States of America
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
; COMPUTER: PC
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: Wordperfect 6.0a WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/598,062
; FILING DATE: 20-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,171

; FILING DATE: <Unknown>
; APPLICATION NUMBER: 60/014,233
; FILING DATE: March 27, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hana VERNY
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: (HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-1677
; TELEFAX: (415) 324-1678
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
; US-09-598-062-14

Query Match 50.9%; Score 29; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WTVRNSW 7
|
Db 2 WIXXNSW 8

RESULT 10

US-08-706-741B-79
; Sequence 79, Application US/08706741B
; Patent No. 5955593
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63146

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,741B
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-706-741B-79

Query Match 46.5%; Score 26.5; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 WT-VRNSWD 8
|
Db 1 WTRIIQSWD 9

RESULT 11
US-08-924-695A-79
; Sequence 79, Application US/08924695A
; Patent No. 5998583
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,695A
; FILING DATE: 09-SEP-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 971798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-924-695A-79

Query Match 46.5%; Score 26.5; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 WT-VRNWD 8
|| : |||
Db 1 WTRIQSWD 9

RESULT 12
US-08-733-505A-42
; Sequence 42, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A

; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-42

Query Match 43.0%; Score 24.5; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 WTVRN-SWD 8
| : |||
Db 1 WKEHNSWD 9

RESULT 13
US-08-706-741B-77
; Sequence 77, Application US/08706741B
; Patent No. 5955593
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63146
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,741B
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-706-741B-77

Query Match 43.0%; Score 24.5; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 WTVRN-SWD 8
| : |||

Db 1 WKEHNRSD 9

RESULT 14

US-08-924-695A-77
; Sequence 77, Application US/08924695A
; Patent No. 5998583
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,695A
; FILING DATE: 09-SEP-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 971798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-924-695A-77

Query Match 43.0%; Score 24.5; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 WTVRN-SWD 8
Db 1 WKEHNRSD 9

RESULT 15

US-09-082-279B-1488
; Sequence 1488, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohmed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1488
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-2

US-09-082-279B-1488

Query Match 42.1%; Score 24; DB 3; Length 8;
Best Local Similarity 42.9%; Pred. No. 4.1e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WTVRNSW 7
Db 1 WDVFSNW 7

Search completed: May 19, 2005, 18:27:15
Job time : 42 secs

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